

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: May 16, 2001, 09:00:12 ; Search time 1134.01 Seconds
(without alignments)
10651.138 Million cell updates/sec

Title: US-09-402-488A-3
Perfect score: 819
Sequence: 1 ATCCGGGTCTCATCATCA.....ATTCCAACTGCACCCCTGTAG 819

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1283235 seqs, 7373929652 residues
Total number of hits satisfying chosen parameters: 2566470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl.*
1: gb_ba1.*
2: gb_ba2.*
3: gb_ba3.*
4: gb_in1.*
5: gb_in2.*
6: gb_in3.*
7: gb_om.*
8: gb_ov.*
9: gb_pat1.*
10: gb_pat2.*
11: gb_ph.*
12: gb_pl1.*
13: gb_pl2.*
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15: gb_pl4.*
16: em_ba1.*
17: em_ba2.*
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19: em_htgo_hum.*
20: em_htgo_inv.*
21: em_htgo_rod.*
22: em_htg_hum1.*
23: em_htg_hum2.*
24: em_htg_hum3.*
25: em_htg_hum4.*
26: em_htg_hum5.*
27: em_htg_hum6.*
28: em_htg_hum7.*
29: em_htg_hum8.*
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85: gb_pr1.*
86: gb_pr2.*
87: gb_pr3.*
88: gb_pr4.*
89: gb_pr5.*
90: gb_pr6.*
91: gb_pr7.*
92: gb_pr8.*
93: gb_pr9.*
94: gb_rol.*
95: gb_rol2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	567	69.2	1164	8	CYIGH M27000 Cyprinus ca
2	528.6	64.5	1117	8	AF069398 Carassius
3	527	64.3	1158	8	CCGH X13670 Cyprinus c
4	509.4	62.2	1179	8	AF069399 Carassius
5	504	61.5	1158	8	HNPGH X60473 H nobilis (
6	502.4	61.3	1170	8	HNPGH X60475 H.multirix
7	501.4	61.2	567	8	CAU28388 Carassius a
8	500.8	61.1	1171	8	CIPGH X60474 C.idellus (
9	496	60.6	1171	8	CTEGRH M27094 Ctenopharyn
10	460.6	56.2	1162	8	AF134200 Labeo roh
11	324.4	39.6	603	8	PNAGH M63713 Pangasius p

Isolation and characterization of two distinct growth hormone cDNAs from the goldfish, *Carassius auratus*
Arch. Biochem. Biophys. 330 (1), 19-23 (1996).
96230236
2 (bases 1 to 1117)
Law, M.S., Cheng, K.W., Fung, T.K., Chan, Y.H., Yu, K.L. and Chan, K.M.
Direct Submission
Submitted (31-MAY-1998) Department of Zoology, The University of Hong Kong, Pokfulam Road, Hong Kong, China
Location/Qualifiers
1. .1117
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1. .633
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298 a 249 c 249 g 321 t
BASE COUNT
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Db				
QY	313	GCTGCAAAAATGATTAACGACTTTGAGGACAGCGCTGTTGCTTGAGGAACGACAGACACTG	372	
Db				
QY	127	GCTGCAAAAATGATTAACGACTTTGAGGACAGCGCTGTTGCTTGAGGAACGACAGACACTG	186	
Db				
QY	373	AGTAAATCTTCCCTCTGCTTCTTCTGCAATCTGACTACATTTGAGGGCGCTGCTGGAAAA	432	
Db				
QY	187	AGTAAATCTTCCCTCTGCTTCTTCTGCAATCTGACTACATCGAGGGCGCACTGGAAAA	246	
Db				
QY	433	GATGAACACAGAAGACTCTATGCTCAAGCTTCTTCGCACTCTCTTTTCACTTCATTGAG	492	
Db				
QY	247	GATGAACACAGAAGACTCTATGTTGAGCTTCTTCGCGTCTCTTTTCGCCCTATTGAG	306	
Db				
QY	493	TCCTGGGAGTTCCCAAGCCAGTCCCTGAGCGGAACCGCTCTCAACAGCCTGACCGTAGGG	552	
Db				
QY	307	TCCTGGGAGTTCCCAAGCCAGACCCCTGAGCGGGACCCGCTCAAAACAGCCTGACCGTCGGC	366	
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QY	553	AACCCCAACAGCTCACTGAGAAGCTGGCGAGCTTGAATGGCATGCGCATCACTGTGCTCATC	612	
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QY	367	AACCCCAACAGATCACTGAGAAGCTGGCGAGCTTGAATGGCATGCGCATCACTGTGCTCATC	426	
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QY	613	CAGGCATGCTCGATGCTCAACCAACATGGATGATTAACGACTCTCTTGCAGCGCTGCTTTT	672	
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QY	427	CAGGCATGCTCGATGCTCAACCAACATGGATGATTAACGACTCTCTTGCAGCGCTGCTTTT	486	
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QY	487	GAGGAATTTCTACTTTGACCATGGGGGATTAACAGCCTTAGAGAGAGCTTTTCGCTGCTGGCT	546	
Db				
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QY	793	TCCCTGGATTCCAAGTCGACCCCTGTAG	819	
Db				
QY	607	TCTTTGGATTCCAAGTCGACCCCTGTAG	633	
Db				

RESULT 3

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CCGH          1158 bp      mRNA          VRT          22-MAR-1995
CYPRINUS CARPIO mRNA for growth hormone.
X13670
X13670.1      GI:62607
growth hormone.
common carp.
CYPRINUS CARPIO
Eukaryota; Metazoa; Chordata; Vertebrata; Actinopterygii;
Neopterygia; Teleostei; Euteleostei; Ostariophysi; Cypriniformes;
Cyprinoidae; Cyprinidae; Cyprininae; Cyprinus.
1 (bases 1 to 1158)
Chang, W.C.
Direct Submission
Submitted (28-NOV-1988) Chang W.C., Institute of Biological
Chemistry, Academia Sinica, PO Box 23-106, Taipei, Taiwan, ROC
2 (bases 1 to 1158)
Chao, S.C.; Pan, F.W. and Chang, W.C.
Purification of carp growth hormone and cloning of the
complementary DNA
Biochim. Biophys. Acta 1007 (2), 233-236 (1989)
89150258      Location/Qualifiers
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23..655
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QY	613	CAGGCATGCTCGATGTGTCAACCAACATGATGATTAACGACTCCTTGCCGCTGCCTTTT	672	

Qy	433	GATGAACACAGAGAGAGCTCTATGCTGAAGCTTCTTTCGCAATCTCTTTTACACCTCATTTGAG	492
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Db	287	GATGAACACAGAGAGAGCTCTATGCTGAAGCTTCTTTCGCAATCTCTTTTACACCTCATTTGAG	346
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Db	527	GAGGACTTCTACTTGACATGCGGGGAGAACCACTCAGAGAGAGCTTTCGCTCTGCTGGCT	586
Qy	733	TGCTTCAAGAGGACATGCACAAAGTGCAGACCTTACTTGAGGGTTGCAAAATGCAGGAGA	792
Db	587	TGTTTAAAGAGGACATGCACAAAGTGCAGACCTTACTTGAGGGTTGCAAAATGCAGGAGA	646
Qy	793	TCCTCGGATTCCAACTGCACCCCTGAG	819
Db	647	TCCTCGGATTCCAACTGCACCCCTGAG	673
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LOCUS		H.nobilis (Bighead carp)	mrna
DEFINITION		H.nobilis (Bighead carp) mrna for growth hormone.	
ACCESSION		X60473	549318
VERSION		X60473.1	GI:65313
KEYWORDS		growth hormone.	
SOURCE		noble carp.	
ORGANISM		Hypophthalmichthys nobilis	
REFERENCE		Huang, F.I.	
AUTHORS		Submitted (09-JUL-1991), F.L. Huang, Institute of Biological	
TITLE		Chemistry, Academia Sinica, P O Box 23-106, Taipei, Taiwan	
JOURNAL		2 (bases 1 to 1158)	
REFERENCE		Chang, Y.S., Liu, C.S., Huang, F.L. and Lo, T.B.	
AUTHORS		The primary structures of growth hormones of three cyprinid	
TITLE		species: bighead carp, silver carp, and grass carp	
JOURNAL		Gen. Comp. Endocrinol. 87 (3), 385-393 (1992)	
MEDLINE		93051159	
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ORIGIN		c	256
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Qy	312	GGCTGCAAAAATGATTAAAGCATTGAGGACAGCGCTGTTGCCTGAGGAAACGACAGACGCT	371		
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Db	394	GAACCCCAACGCTCTACTGAGAGCTGGCGGACTTCAAAATGGGCATCAGTGTGCTCAT	453		
Qy	612	CCAGGCATGTCTCGATGGTCAACCAACATGATGATGATGATGATGATGATGATGATGATGAT	671		
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Db	514	TGAGGACTTCTACTTGACCATGGGGGAGAGAGAGCTTCTGCTGTGCGCTTCTGCTGCG	573		
Qy	732	TTGCTTCAAGAGACATGCACAAAGTCGAGACCTACTTTCAGGGTTGCAAAATTCGAGGAG	791		
Db	574	TTGCTTCAAGAGACATGCACAAAGTCGAGACCTACTTTCAGGGTTGCAAAATTCGAGGAG	633		
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29. .661

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BASE COUNT

312 a 272 c 259 g 327 t

ORIGIN

RESULT 7

CAU28388

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

CAU28388

567 bp

mRNA

Carassius auratus growth hormone mRNA, partial cds.

U28388

GI:1143868

goldfish.

Carassius auratus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Cyprininae; Carassius.

1 (bases 1 to 567)

AUTHORS Mahmood, S.S., Moloney, M.M. and Habibi, H.R.
 TITLE Cloning and sequencing of the goldfish growth hormone cDNA
 JOURNAL Gen. Comp. Endocrinol. 101 (2), 139-144 (1996)
 MEDLINE 96271507
 REFERENCE 2 (bases 1 to 567)
 AUTHORS Mahmood, S.S.
 TITLE Direct Submission
 JOURNAL Submitted (05-JUN-1995) Scheil S. Mahmood, Biological Sciences,
 University of Calgary, 2500 University Drive NW, Calgary, AB, T2N
 1N4, Canada

FEATURES

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 Db 361 AAGGAGTCTCGATGTTCAACCAACATGATGATACGACTCTCTGCGGCTGCCTTTT 420
 QY 673 GAGGATCTCTACTTACCATGGGGAGAACACCTTCAGAGAGCTTTTCTGCTGGCTGGCT 732
 Db 421 GAGGATCTCTACTTACCATGGGGAGAACACCTTCAGAGAGCTTTTCTGCTGGCTGGCT 480
 QY 733 TGCTTCAAGAGGAGATGCACAAAGTCGAGACCTACTTTGAGGGTTGCAAAATTCGAGGAGA 792
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 QY 793 TCCCTGGATTCCAACTGCACCCCTGTAG 819
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RESULT 8

CIPGH 1171 bp mRNA VRT 14-JUN-1994
 LOCUS C.idellus (Grass carp) mRNA for growth hormone.
 DEFINITION X60474
 ACCESSION X60474.1 GI:62710
 VERSION growth hormone.
 KEYWORDS growth hormone.
 SOURCE grass carp.
 ORGANISM Ctenopharyngodon idella
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 Neopterygii; Euteleostei; Euteleostei; Ostariophysi; Cypriniformes;
 Cyprinidae; Cyprinidae; Cyprinidae; Cyprinidae; Ctenopharyngodon.
 Huang, F.I.
 REFERENCE 1 (bases 1 to 1171)
 AUTHORS Direct Submission
 TITLE Submitted (09-JUL-1991) F.L. Huang, Institute of Biological
 JOURNAL Chemistry, Academia Sinica, P O Box 23-106, Taipei, Taiwan
 2 (bases 1 to 1171)
 REFERENCE Chang, Y.S., Huang, F.I. and Lo, T.B.
 AUTHORS The cDNA and primary structure of pregrowth hormones of three
 TITLE species of Cyprinidae: silver carp, bighead carp and grass carp
 JOURNAL Unpublished
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BASE COUNT 320 a 267 c 256 g 328 t
 ORIGIN

Query Match 61.1%; Score 500.8; DB 8; Length 1171;
 Best Local Similarity 92.6%; Pred. No. 1.3e-127;
 Matches 526; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

QY 252 CTCAGACACACGAGCGCTCTTCAATAATGACGTCATTCGTGTACACACCTGCACAGCT 311
 Db 89 CTCAGACACACGAGCGCTTTTCAACACGAGTCATCCGTTTCAACACCTGCACAGCT 148
 QY 312 GGTGCAAAATGATTAAACGACTTTGAGGACAGCTTTCCTGCTGAGGAGCGACAGCT 371
 Db 149 GGTGCAAAATGATTAAACGACTTTGAGGACAGCTTTCCTGCTGAGGAGCGACAGCT 208
 QY 372 GAGTAAATCTTCCCTCTGCTTTCGCAATCTGACTACATTCGAGCGCTGCTGGAATA 431
 Db 209 GAGTAAATCTTTCCTGCTTTCGCAATCTGACTACATTCGAGCGCGCTGCTGGAATA 268
 QY 432 AGATGAACACAGAGAGCTCTATGCTGAAGCTTCTTCGCATCTCTTTTACCTCATTTGA 491
 Db 269 AGATGAACACAGAGAGCTCTATGCTGAAGCTTCTTCGCATCTCTTTTACCTCATTTGA 328
 QY 492 GTCCTGGGAGTTCCCAAGCCAGTCCCTGAGCGGAACCGTCTCAACAGCTGACCGTAGG 551
 Db 329 GTCCTGGGAGTTCCCAAGCCAGTCCCTGAGCGGAACCGTCTCAACAGCTGACCGTAGG 388
 QY 552 GAACCCCAACGAGCTCACTGAGAGCTGCCGAGCTTGAATGGCATGCTGCTCAT 611
 Db 389 GAACCCCAACGAGCTCACTGAGAGCTGCCGAGCTTGAATGGCATGCTGCTCAT 448
 QY 612 CCAGGATCTGCTGATGGTCAACCAACATGATGATGATGATGATGATGATGATGATGATGAT 671
 Db 449 CAAGGATCTGCTGATGGTCAACCAACATGATGATGATGATGATGATGATGATGATGATGAT 508

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QY 672 TGAGGACTTCTACTTACCATTGGGAGAGAACCTCAGAGAGAGCTTTCTGCTGCTGGC 731
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Db 509 TGAGGATTCTTACTTAACCATGGGAGAGACCCCTCAGAGAGAGCTTTCTGCTTCTGGC 568
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QY 732 TTGCTTTCAAGAAGGACATGCACAAAGTCGAGACCTACTTCTGAGGGTTGCAAAATTCGAGGAG 791
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QY 792 ATCCCTGGATTCCAACTGCACCTGTAG 819
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Db 629 ATCCCTGGATTCAAACTGCACCTGTAG 656
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RESULT 9
CTEGRH CTEGRH 1171 bp mRNA VRT 03-JAN-1995
LOCUS Ctenopharyngodon idella growth hormone mRNA, complete cds.
DEFINITION M27094
ACCESSION M27094
VERSION M27094.1 GI:609443
KEYWORDS growth hormone.
SOURCE Ctenopharyngodon idella pituitary gland cDNA to mRNA.
ORGANISM Ctenopharyngodon idella
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Cyprininae; Ctenopharyngodon.
REFERENCE 1 (bases 1 to 1171)
AUTHORS Ho,W.K., Tsang,W.H. and Dias,N.P.
TITLE Cloning of the grass carp growth hormone cDNA
JOURNAL Biochem. Biophys. Res. Commun. 161 (3), 1239-1243 (1989)
MEDLINE 89302103
COMMENT On Jan 4, 1995 this sequence version replaced gi:341636.
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                    /protein_id="AAA58724.1"
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sig_peptide 44..100
mat_peptide 101..670
polyA_signal 1154..1159
BASE COUNT 313 a 270 c 259 g 329 t
ORIGIN

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Best Local Similarity 92.1%; Pred. No. 2.8e-126;
Matches 523; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

QY 252 CTCAGACAAACCGCGCTCTCAATAATGACGTCATTCGTGTACACACACCTGCACACGCT 311
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Db 109 CTCAGACAAACCGCGCTCTCAACACACGTCATTCGTGTACACACCTGCACACGCT 168
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QY 312 GCCTCAAAATGATTACGCTTTGAGGACAGCGCTGTTCCTCGTGAGGACGACGACGCT 371
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Db 169 GCCTCAAAATGATTACGCTTTGAGGACAGCGCTGTTCCTCGTGAGGACGACGACGCT 228
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QY 432 AGATGAACACAGAGAGCTCTATGCTGAAGCTTCTTCGATCTCTTTCACTCATTTGA 491
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Db 289 AGATGAACACAGAGAGCTCTATGCTGAAGCTTCTTCGATCTCTTTCCGCTCATTTGA 348
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Db 349 GTCCCTGGAGTTCCCAAGCCAGTCCCTCAGCGGACCCCTCTCAACAGCCTACCGTAG 408
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QY 552 GAACCCCAACAGCTCACTGAGAAAGTGGCGACTTTGAAAATGGGCATCAGTGTGCTCAT 611
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Db 469 CAAGGATGCTGTGATGGTCAACCAACATGGATGATTAACGACTCCTTGGCCGCTGCTTT 528
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QY 672 TGAGGACTTCTACTTGACCATGGGAGAAACCACTCAGAGAGAGCTTTCTGCTGCTGCG 731
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QY 732 TTGCTTCAAGAAGGACATGCACAAAGTCGAGACCTTACTTTGAGGGTTGCAAAATTCGAGGAG 791
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Db 589 TTGCTTCAAGAAGGACATGCACAAAGTCGAGAACTTACCTGAGGGTTGCAAAATTCGAGGAG 648
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QY 792 ATCCCTGGATTCCAACTGCACCTGTAG 819
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Db 649 ATCCCTGGATTCCAACTGCACCTGTAG 676
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RESULT 10
AF134200
LOCUS Labeo rohita growth hormone precursor, mRNA, complete cds.
DEFINITION AF134200
ACCESSION AF134200
VERSION AF134200.1 GI:4836724
KEYWORDS Labeo rohita.
SOURCE Labeo rohita.
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Cyprininae; Labeo.
REFERENCE 1 (bases 1 to 1162)
AUTHORS Venugopal,T., Pandian,T.J. and Mathavan,S.
TITLE Labeo rohita (Indian major carp) growth hormone cDNA, complete cds
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1162)
AUTHORS Venugopal,T., Pandian,T.J. and Mathavan,S.
TITLE Direct Submission
JOURNAL Submitted (09-MAR-1999) Department of Genetics, Madurai Kamara]
University, School of Biological Sciences, Madurai, TN 625 021,
India
FEATURES
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mat_peptide 115..669
polyA_signal 1140..1145
polyA_site 1162
BASE COUNT 321 a 256 c 249 g 336 t
ORIGIN

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Best Local Similarity 89.8%; Pred. No. 1.7e-116;
Matches 509; Conservative 0; Mismatches 49; Indels 9; Gaps 1;

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ACCESSION L27835
 VERSION L27835.1 GI:450294
 KEYWORDS growth hormone.
 SOURCE Pangasianodon gigas cDNA to mRNA.
 ORGANISM Pangasianodon gigas
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
 Siluriformes; Pangasiidae; Pangasianodon.
 REFERENCE 1 (bases 1 to 1176)
 AUTHORS Lemaire, C., Warit, S. and Panyim, S.
 TITLE Giant catfish Pangasianodon gigas growth hormone-encoding cDNA:
 cloning and sequencing by one-sided polymerase chain reaction
 JOURNAL Gene 149 (2), 271-276 (1994)
 MEDLINE 95047487
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 Location/Qualifiers
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 Best Local Similarity 75.9%; Pred. No. 7.4e-79;
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 QY 256 GACAACGAGGGCTCTTCAATATGAGTCATTCGGTGTACACACCTGCACCGCTGGCT 315
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 Db 248 AGATTTTCCCTCTGCTTCTTCTGCACTCGGACTCCATCGAAGCTCTCGCAGGCAAGAC 307
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 QY 496 TGGGAGTTCCCAAGCCAGTCCCTTGAGCGGAACCGCTCTCAACACCGCTTGACCGTAGGGAAC 555
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 QY 556 CCCAACCACTCACTGAGAGCTGGCGGACTTGAATATGGGCATCAGTGTGCTCATCCAG 615
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Db 398 CCCAACCACTCTCAGAGAAGCTGGCTGACCTGACCTGAAATGGGCATCGGCTGCTTATCGAG 457
 QY 616 GCATGCTCTCGATGGTCAACCAACATGATGATAACGACTCTTCGCGCTGCTTTTGTAG 675
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 Db 458 GGATGTTGGATGAGCAACACCGCTGATGAGAACGACTCTCTGCTCCGCCCTTCGAG 517
 QY 676 GACTTCTACTTGACCATGGGGGAGAACACCTCAGAGAGAGCTTTCGCTGCTGCTGCTGC 735
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 Db 518 GATTTCTACCAGACTTTCAGCGAGGGAACCTTGAGGAAGAGCTTCGCTGCTGCTGCTGC 577
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 Db 578 TTCAGAGGACATGCACAAAGTCGAGACCTTCTTTCGAGGGTTCGAAATTCGAGGAGATCC 637
 QY 796 CTGGATTCCAACTGCACCCCTGTAG 819
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 Db 638 CTGGATTCCAACTGCACCCCTGTAG 661
 RESULT 13
 AF147792 1132 bp mRNA VRT 30-MAY-1999
 LOCUS AF147792 Heteropneustes fossilis growth hormone (GH) mRNA, complete cds.
 DEFINITION AF147792
 ACCESSION AF147792
 VERSION AF147792.1 GI:4927275
 KEYWORDS Heteropneustes fossilis.
 SOURCE Heteropneustes fossilis.
 ORGANISM Heteropneustes fossilis
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
 Siluriformes; Siluridae; Heteropneustes.
 REFERENCE 1 (bases 1 to 1132)
 AUTHORS Anathy, V., Pandian, T.J. and Mathavan, S.
 TITLE Heteropneustes fossilis growth hormone mRNA
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 1132)
 AUTHORS Anathy, V., Pandian, T.J. and Mathavan, S.
 TITLE Direct Submission
 JOURNAL Submitted (02-MAY-1999) Genetics, Madurai Kamaraj University,
 School of Biological Sciences, Madurai, TN 625 021, India
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 Location/Qualifiers
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 59..661
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 Best Local Similarity 74.6%; Pred. No. 9.2e-76;
 Matches 421; Conservative 0; Mismatches 113; Indels 30; Gaps 1;
 QY 256 GACAACGAGGGCTCTTCAATATGAGTCATTCGGTGTACACACCTGCACCGCTGGCT 315

AUTHORS Trofimova, I.N.
Direct Submission
TITLE Submitted (25-JAN-1994) I.N. Trofimova, Limnological Institute,
JOURNAL Irkutsk 664033, PO Box 4199, Russia, USSR
FEATURES Location/Qualifiers
source 1. .742
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Matches 406; Conservative 0; Mismatches 152; Indels 12; Gaps 2;
QY 256 GACAAACAGCGGCTCTTAATATGAGTTCGTCAGTTCGTCACACACCTGCACACGCTGGCT 315
DB 108 GAAACCAACGGCTCTTCAACATCGCAGTCAACCGGGTGCACATCTCCACCTAATGGCT 167
QY 316 GCATAAATGATTACGACCTTTAGGACAGCCTGTTGCCTGAGGAGCAGCAGACGCTGAGT 375
DB 168 CAGAAAATGTTCAATGACTTTGAAGGACCCCTGTTGCTGATGAGCAGCAGACGCTGAAC 227
QY 376 AAAATCTCCCTCTGCTTCTTCATTTCTGACTATGACTGAGCGGCTGCTGAAAAGAT 435
DB 228 AAGATATTCTGCTGACTCTGTAATCTGACTTCCATCTGAGCCCAATTGACAAGCTT 287
QY 436 GAAACACAGAAGCTCTATGCTGAAGCTTCTTCGATCTCTTTTCACCTCATTGAGTCC 495
DB 288 GAGATCAGAAGAGTTCAGTCTGAGAGCTGCTCCATATCTCTTCGCTGATTGAATCA 347
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DB 348 TGGGAGTACCTTAGCCAGACCCCTG-----ACCATCTCCAACAGTCTAATGGTCAGAAAC 401
QY 556 CCCAACCACTCAGTGAAGCTGGCCGAGCTTGAATAATGGGCATCAGTGTGCTCATCCAG 615
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DB 522 GGAACACTACTACCAAGACCTGGGGGGCGAGCGCAACGTCAGGAGGAACTACGAGCTGTTG 581
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DB 582 GCCTGCTTCAAGAAGGACATGCACAAGTCGAGACCTACTGACCGTTGCCAAGTCGAGG 641
QY 790 AGATCCCTGGATTCCCAACTGCACCTGTAG 819

Db 642 AAGTCACTGGAGGCCAACTGCACCTCTGTAG 671
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Job time: 3753 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: May 16, 2001, 09:22:47 ; Search time 127.22 Seconds
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Perfect score: 819
Sequence: 1 ATCGGGGTTCTCATCATCA.....ATTCCAACTGCACCTGTAG 819

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 678276 seqs, 291890651 residues

Total number of hits satisfying chosen parameters: 1356552

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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5	278.6	34.0	1176	14	Q38832
6	278.6	34.0	1201	16	Q98905
7	277.6	33.9	633	11	Q06417
8	277	33.8	633	7	N60340
9	275.6	33.7	564	8	N70829
10	275.4	33.6	1119	13	Q29359
11	273.8	33.4	633	11	Q06132

12	270.6	33.0	633	11	Q06131	Sequence encoding
13	217	26.5	555	12	Q10874	plasmid pMWTfw1 co
14	203.2	24.8	630	8	N70544	Eel growth hormone
15	203.2	24.8	630	9	N81504	cDNA encoding GH-1
16	183.8	22.4	564	9	N80701	Sequence encoding
17	169.4	20.7	887	11	Q06743	Insert from ptIGH6
18	167.8	20.5	887	11	Q05160	Fragment of plasmid
19	167	20.4	5108	21	288226	Misgurnus mizolepi
20	166.4	20.3	337	14	Q36414	plasmid PSGHE1 fra
21	166.4	20.3	381	14	Q36415	plasmid PSGHEC-1 f
22	166.4	20.3	414	14	Q36422	plasmid PSGHEC-14B
23	166.4	20.3	429	12	Q14067	HCV detecting pept
24	166.4	20.3	429	14	Q36416	plasmid PSGHEC-14
25	166.4	20.3	429	14	Q36421	plasmid PSGHEC-14A
26	166.4	20.3	516	14	Q36417	plasmid PSGHEC-18
27	166.4	20.3	537	12	Q14066	HCV detecting pept
28	166.4	20.3	537	14	Q36418	plasmid PSGHEC-141
29	166.2	20.3	942	10	N90111	Fish growth hormon
30	164.8	20.1	337	12	Q14062	HCV detecting pept
31	164.8	20.1	381	12	Q14063	HCV detecting pept
32	164.6	20.1	944	12	Q10912	Fish growth hormon
33	163.2	19.9	414	12	Q14068	HCV detecting pept
34	161.6	19.7	429	12	Q14064	HCV detecting pept
35	157.2	19.2	576	9	N81780	Sequence of synthe
36	156.8	19.1	516	12	Q14065	HCV detecting pept
37	156.2	19.1	576	4	N30046	Sequence of synthe
38	154	18.8	714	21	A54214	Synthetic construc
39	153.2	18.7	608	10	N90364	Fish growth hormon
40	152.4	18.6	576	9	N80724	Cattle somatotropi
41	152.4	18.6	601	11	Q05662	EK-bovine growth h
42	152.4	18.6	601	12	Q10188	EK-bovine growth h
43	152.4	18.6	601	14	Q38308	Plasmid EK-bGH. S
44	152.4	18.6	601	14	Q42407	Bovine growth Horm
45	152.4	18.6	601	14	Q43934	EK-BGH (Metpheprol

ALIGNMENTS

RESULT 1
V83967
ID V83967 standard; DNA; 819 BP.
XX
AC V83967;
XX
DT 09-MAR-1999 (first entry)
XX
DNA encoding His-chymosin pro-peptide-carp growth hormone.
DE
XX
Fusion protein; bovine chymosin pro-peptide; leech hirudin;
KW antioagulant protein; autocatalytically maturing zymogen;
KW carp growth hormone; vaccine; ss.
XX
XX Synthetic.
OS Bos sp.
OS Cyprinus carpio.
XX
FH Key Location/Qualifiers
FT CDS 1..819
FT FT /tag= a
FT FT /product= His-chymosin_pro-peptide-carp_growth_hormone
FT FT /tag= b
FT FT /note= "encodes bovine chymosin pro-peptide"
FT FT 253..816
FT FT /tag= c
FT FT /note= "carp growth hormone"

WO9849326-A1.
XX
05-NOV-1998.
XX
23-APR-1998; 98WO-CA00398.

Matches 410; Conservative 0; Mismatches 149; Indels 12; Gaps 3;

QY 255 AGACAACACGCGGCTCTCAATATGAGTCAATTCGTTGTAACAACACCTGCACACGCTGGC 314
 Db 111 agaaagcaacgctctcaacatcggtcagcgtgtgcaacatctccaccattggc 170
 QY 315 TGCATAAATGATTAAACAGCTTTGAGGACAGCCTGTTGCCTGAGGAACGACAGCTGAG 374
 Db 171 tcagaaatgttcaatgacttgcaggtacccctgttgcctgagtgaagcgcagacagctgaa 230
 QY 375 TAAATCTCCCTCTGCTTCTGCAATTCGACTGACTAGCTGAGCGGCTGCTGGAAGA 434
 Db 231 caagatatctctgctggaactctgcaactctgactccatctgagcccaatcgacaagca 290
 QY 435 TGAACACAGAGAAGCTCTATGCTGAAGCTTCTTCGCACTCTCTTTTACCTCACTTGAAGTC 494
 Db 291 cgagactcagaagagttcagctcctgaagctgctccatctcttccgtgattgattc 350
 QY 495 CTGGGAGTTCCCAAGCAGTCCCTGAGCGGAACCGTCTCAAAACAGCCTGACCGTAGGAA 554
 Db 351 ctgggagttaccctagccagaccctg-----atcatctcaacagcctaattggtcagaaa 404
 QY 555 CCCCACACAGCTCAGTCAAGAGCTGGCCGAGCTTGAATAAGGCAATGAGTGTGCTCATCCA 614
 Db 405 cgccaaacagatctctgagaagctcagcgaccccaagtggtgcatcaatctgctcatcac 464
 QY 615 GGCATGCTCTGATGGTCAACCAACATGAGTATGATGATGATGATGATGATGATGATGATG 671
 Db 465 ggggaacacagagtggtgactgagcctggatgacaaagctcagcagcctgcccccta 524
 QY 672 TGAGGACTTCTTACTTGACCATGGGGGAGAAC---AACTCAGAGAGAGCTTTCGCTGCT 728
 Db 525 cgggaaactactaccagaacctggggggcgagaaacgtcaggaggaactacagagttgtt 584
 QY 729 GGCCTTCTCAAGAGGACATGACAAAGTCGAGACCTACTTGAAGGTTGCAATTCGAG 788
 Db 585 ggtctgttcaagaagagacatgacaaaggtcgagacactgacacgtgacacgtgacag 644
 QY 789 GAGATCCCTGGATTCAACATGCAACCTGACCTGTAG 819
 Db 645 gaagtcactggaggccaactgactctgtag 675

RESULT 6

Q98905

ID Q98905 standard; DNA; 1201 BP.

XX Q98905;

AC Q98905;

XX Q98905;

DT 11-MAR-1996 (first entry)

XX Coho Salmon growth hormone gene.

XX Coho Salmon growth hormone gene.

XX Coho Salmon growth hormone gene.

XX Coho Salmon growth hormone gene.

XX Coho Salmon growth hormone gene.

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05-AUG-1994; 94US-0286872.

04-FEB-1994; 94US-0191494.

04-FEB-1994; 94US-0192272.

(MADS/) MADSEN A L.

(STRD) UNIV LELAND STANFORD JUNIOR.

Gomez-chiarri M, Hereford L, Powers D, Madsen AL;

WPI; 1995-283542/37.

P-PSDB; R80623.

New transgenic molluscs, esp. abalone - contg. a DNA sequence

heterologous to the mollusc, esp. for enhancing growth properties

Example 1; Page 37; 6lpp; English.

This sequence represents the coho salmon growth hormone gene (csGH).

This sequence was included in a vector used to create transgenic molluscs

(especially abalone). In the vector pLH2 this sequence is under the

control of the actin promoter ACT5-C. This vector increased the growth

of the transgenic abalone. Transgenic molluscs created in this manner

can be used to carry DNA whose product promotes growth enhancement,

e.g. a gene encoding a growth factor esp. an insulin-like growth factor.

Sequences whose product affects the taste or texture of mollusc tissue

can also be introduced in this way. Polyploid organisms can be created

by treating the fertilised egg with cytochalasin B. If the fertilised

egg is diploid the resulting polyploids are triploid or tetraploid.

These polyploid organisms have enhanced growth properties relative to the

same organism with a normal chromosome complement. Triploids allow for

the production of sterile seed stock, thereby overcoming environmental

concerns.

Sequence 1201 BP; 329 A; 274 C; 267 G; 331 T; 0 other;

Query Match 34.0%; Score 278.6; DB 16; Length 1201;

Best Local Similarity 71.8%; Pred. No. 6e-70;

Matches 410; Conservative 0; Mismatches 149; Indels 12; Gaps 3;

QY 255 AGACAACACGCGGCTCTTCAATAATGAGTCAATTCGTTGTAACAACACCTGCACACGCTGGC 314

Db 133 agaaacacacgctcttcaacatcggtcagcgtgtgcaacatctccaccattggc 192

QY 315 TGCATAAATGATTAAACAGCTTTGAGGACAGCCTGTTGCCTGAGGAACGACAGCTGAG 374

Db 193 tcagaaatgttcaatgacttgcaggtacccctgttgcctgagtgaacgcagacagctgaa 252

QY 375 TAAATCTCCCTCTGCTTCTGCAATTCGACTGACTAGCTGAGCGGCTGCTGGAAGA 434

Db 253 caagatatctctgctggaactctgcaactctgactccatctgagcccaatcgacaagca 312

QY 435 TGAACACAGAGAAGCTCTATGCTGAAGCTTCTTCGCACTCTCTTTTACCTCACTTGAAGTC 494

Db 313 cgagactcagaagagttcagctcctgagcgtgctccatcttcttccgtctgattgattc 372

QY 495 CTGGGAGTTCCCAAGCAGTCCCTGAGCGGAACCGTCTCAAAACAGCCTGACCGTAGGAA 554

Db 373 ctgggagttaccctagccagaccctg-----atcatctcaacagcctattggtcgga 426

QY 555 CCCCACACAGCTCAGTCAAGAGCTGGCCGAGCTTGAATAAGGCAATGAGTGTGCTCATCCA 614

Db 427 cgccaaacagatctctgagaagctcagcgaccccaagtggtgcatcaatctgctcatcac 486

QY 615 GGCATGCTCTGATGGTCAACCAACATGAGTATGATGATGATGATGATGATGATGATG 671

Db 487 ggggagcagagtggtcctgactgagcctggatgacaaatgactctcagcagcgtcccgcta 546

QY 672 TGAGGACTTCTTACTTGACCATGGGGGAGAAC---AACTCAGAGAGAGCTTTCGCTGCT 728

Db 547 cgggaactactaccagaacctggggggcgagaaacctgagggaggaactacagttgtt 606

Qy 729 GCTTGTCTCAAGAGGACATGCACAAAGTCGAGACCTACTTGAGGGTTGCAAAATTGCAG 788
 |||||
 Db 607 gcttgcctcaagaaggacatgcacaaagtcgagaccctaccctgacgcctgcgccaagtgcag 666
 |||||
 Qy 789 GAGATCCCTGGATTCCAACTGCACCTCTAG 819
 |||||
 Db 667 gaagtcactggaggccaactgcactctgtag 697
 |||||
 RESULT 7
 Q06417
 ID Q06417 standard; DNA; 633 BP.
 XX
 AC Q06417;
 DT 05-FEB-1991 (first entry)
 DE Sequence encoding rainbow trout Growth hormone GH2.
 XX
 KW Fish growth hormone; salmon; FGH; SGH; ds.
 XX
 OS Salmo gairdneri.
 XX
 PN JP02243700-A.
 XX
 PD 27-SEP-1990.
 XX
 PF 17-MAR-1989; 89JP-0063594.
 XX
 PR 17-MAR-1989; 89JP-0063594.
 XX
 PA (NIUS) NIPPON SUISAN KAISHA.
 XX
 DR WPI; 1990-338513/45.
 DR P-PSDB; R07642.
 XX
 FT Growth hormone gene of fish - contains polypeptide with specific
 PT aminoacid sequence
 XX
 PS Disclosure; Fig 1; 8pp; Japanese.
 XX
 CC Fish growth hormone may be used to accelerate growth in cultured
 CC fish.
 XX
 SQ Sequence 633 BP; 165 A; 176 C; 157 G; 135 T; 0 other;
 Query Match 33.9%; Score 277.6; DB 11; Length 633;
 Best Local Similarity 71.8%; Pred. No. 9e-70;
 Matches 409; Conservative 0; Mismatches 149; Indels 12; Gaps 3;
 Qy 256 GACACACGCGGCTCTTCAATAATGAGTCATTCGTGTACACACCTGCACCGAGTGGCT 315
 |||||
 Db 70 gaaacacacgctcttcaacacgcggtcgaatccgctgcaacacacccctaccctattggct 129
 |||||
 Qy 316 GCAAAATGATTAAAGCACTTTGAGACAGCCCTGTCCTGAGAACGCGAGACGCTGACT 375
 |||||
 Db 130 cagaaatgttcaacgactttgaagcaccctgttgcctgtagaacgcagacagctgaac 189
 |||||
 Qy 376 AAAATCTTCCTCTCTCTTCTGCAATTCGACTACATTCGAGCGGCTGCTGCAAAAGAT 435
 |||||
 Db 190 aagatatctcctgctggaactctgtgaactctgactcctcctgtagcccaatcgacaagcag 249
 |||||
 Qy 436 GAAACACAGAGAGCTCATGTGAGCTTCCTGCGATCTTCGATCTTTTCACCTCATTTAGTCC 495
 |||||
 Db 250 gagactcagaagagttcagctcctgaagctgctccacatttcttccgctgattgaatcc 309
 |||||
 Qy 496 TGGGAGTTCACAGCAGTCCCTGAGCGGAACCGTCTCAACAGCGCTGACCGTAGGGAC 555
 |||||
 Db 310 tgggagtagccttagcagaccctg-----accattcccaacgacgctaattggtcagaaac 363
 |||||
 Qy 556 CCCAACCGAGCTCAGTGAGAGAGCTGGCCGCACTTGAATGGCATCAGTGTGCTCATCCAG 615
 |||||

Db 364 tccaaccagatctctgagaagctcagcaccctcaaaagtgggcatcaacccgtctcatcaag 423
 Qy 616 GCATGCTCGATGGTCAACCAACATGATGATGAACAGACTCTCTTGGCGCTG---CCTTTT 672
 |||||
 Db 424 gggagccagatggcgctactaagcctggatgacaatgactctcagcatctgccccctac 483
 |||||
 Qy 673 GAGGACTTCTACTTTGACCATGGGG---GAGAACAACTCAGAGAGAGCTTTGCTGCTGTG 729
 |||||
 Db 484 gggaaactactaccagaacctggggcgacg9caacgctcagggaggaactacgagctgttg 543
 |||||
 Qy 730 GCTTGTCTCAAGAAGGACATGCACAAAGTCGAGACCTACTTGAGGGTTGCAAAATTGCAG 789
 |||||
 Db 544 gcatgcttcaagaagtacatgataaggttgagacctacctgacccgtcgccaagtgcag 603
 |||||
 Qy 790 AGATCCCTGGANTCCAACTGCACCCCTGTAG 819
 |||||
 Db 604 aagtatctggaggccaactgcactctgtag 633
 |||||
 RESULT 8
 N60340
 ID N60340 standard; DNA; 633 BP.
 XX
 AC N60340;
 DT 13-JUN-1991 (first entry)
 DE Sequence encoding salmon growth hormone variant of plasmid pSGH1.
 XX
 KW SGH; E.coli; ds.
 XX
 OS Oncorhynchus keta.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..633
 FT /*tag= a
 XX
 PN EP166444-A.
 XX
 PD 02-JAN-1986.
 XX
 PF 27-JUN-1985; 85EP-0107987.
 XX
 PR 13-MAR-1985; 85JP-0050096.
 PR 29-JUN-1984; 84JP-0134536.
 PR 12-OCT-1984; 84JP-0213360.
 PR 12-OCT-1984; 84JP-0213361.
 XX
 PA (KYOW) KYOWA HAKKO KOGYO KK.
 PA (SEKI/) SEKINE S.
 XX
 PI Sekine S, Mizukami T, Sato M, Itoh S, Saito A;
 XX
 DR WPI; 1986-008665/02.
 DR P-PSDB; P60322.
 XX
 PT Fish growth hormone poly-peptide - produced by culturing
 PT microorganisms carrying recombinant DNA plasmid.
 XX
 PS Claim 1; Table 2; 32pp; English.
 XX
 CC The two variants of salmon growth hormone (pSGH1 and pSGH14) may be
 CC expressed from an E.coli host, and used for stimulating growth in
 CC cultivated fish.
 XX
 SQ Sequence 633 BP; 164 A; 172 C; 162 G; 135 T; 0 other;
 Query Match 33.8%; Score 277; DB 7; Length 633;
 Best Local Similarity 71.6%; Pred. No. 1.3e-69;
 Matches 409; Conservative 0; Mismatches 150; Indels 12; Gaps 3;
 Qy 255 AGACACACGCGGCTCTTCAATAATGAGTCATTCGTGTACACACCTGCACCGAGTGGC 314

Db 69 agaaacacacggccttcaacatcgctgagtcgggtgcaacatctccacattg9g 128
Qy 315 TGCACAAATGATTACGACTTTGAGGACAGCTGTGGCTCGAGGACGACGAGCTGAG 374
Db 129 tcagaaatgttcaatgactttgacggtaccctgttgctgatgaaacgacagactgaa 188
Qy 375 TAAATCTCCCTCTGCTCTGCTTTGCAATCTGACTACATTTGAGGCGCTGCTGGAAGA 434
Db 189 caagatattctctggaacttctgaaactgactccatctgagccagtcgacaagca 248
Qy 435 TGAACACAGAGAGCTCTATGCTGAAGCTTCTTCGATCTCTTTTCACTCTATTTGAGTC 494
Db 249 cgagactcagaagagttcagtcctgaagctgtccacatttcttccgtctgattgaatc 308
Qy 495 CTGGAGTTTCCCAAGCAGCTGCTGAGCGGAACCGTCTCAAAACAGCCTGACCGTAGGGAA 554
Db 309 ctggagagtaccctagccagaccctg-----atcaactccacagcctaatggtcagaa 362
Qy 555 CCCCACACAGCTACTGAGAGCTGGCCGACTTGAAAATGGGCATCAGTGTGCTCATCCA 614
Db 363 cgcaaccagatctctgagaagctcagcgacctcaagtggtgcatcaacctgctcatcac 422
Qy 615 GGCATGCTCGATGCTCAACCAACATGATGATACGACTCTCTGCGCGCTG---CCTTT 671
Db 423 ggggagccaggtggtgactgagctggtgatgacaatgactctcagcagctgccccctta 482
Qy 672 TGAGGACTTCTACTTGACCATGGGGAGAAC---AACCTCAGAGAGAGCTTTGCTGCT 728
Db 483 cgggaactactaccagaacctgggggagcagcgaacgtcagaggaaactacgagttgtt 542
Qy 729 GCGTTGCTTCAAGAGGACATGCACAAAGTCGAGACCTACTTGAGGGTTGCAAAATTCGAG 788
Db 543 ggcattctcaagaaggacatgcacaaggtcagacctactctgacctgacgctcgaagtgcag 602
Qy 789 GAGATCCCTGGATCCAACTGCACCCCTGTAG 819
Db 603 gaagtcactggaggccaactgcactctgtag 633

RESULT 9

N70829
ID N70829 standard; DNA; 564 BP.
AC N70829;
XX
XX
DT 13-JAN-1991 (first entry)
DE DNA encoding fish growth hormone.
DE Fish growth hormone; ss DNA; E.coli; plasmid pGEL1.
KW
XX
XX
FH Key Location/Qualifiers
FT 1..564
FT CDS /*tag= a
XX
XX JP6225500-A.
PN
XX
XX 07-NOV-1987.
PD
XX
XX 25-NOV-1986; 86JP-0J97842.
PF
XX
XX 25-APR-1986; 86JP-0097842.
PR
XX
XX (KYOW) KYOWA HAKKO KOGYO KK.
PA
XX
XX WPI; 1987-352166/50.
XX
XX P-PSDB; P70503.
DR
XX
XX

Fish growth hormone polypeptide deriv. - prepd. by culturing
microorganism transformed with recombinant DNA fragment.
Disclosure; Fig. 1 page 861; 11pp; Japanese.

XX Using the DNA, large amts. of fish growth hormone can be produced.
CC The DNA is inserted into a plasmid which can be expressed in E.coli,
CC eg pGEL1. The DNA is suitably the one shown, with bases 58-69
CC deleted. E.coli contg. pGEL1 is deposited as FERM BP-629.
CC It is cultivated at pH 5.5 - 8.5 at 18 - 40 deg C under aeration
CC and stirring.
XX
SQ Sequence 564 BP; 151 A; 160 C; 139 G; 114 T; 0 other;

Query Match 33.7%; Score 275.6; DB 8; Length 564;
Best Local Similarity 71.7%; Pred. No. 3.2e-69;
Matches 407; Conservative 0; Mismatches 149; Indels 12; Gaps 3;

Qy 255 AGACAACCCAGCGCTCTTCAATATGAGTCAGTCATTCTGCTGTAACAACACCTGCAACAGCTGGC 314
Db 3 agaaaacacacgctctccacatcgctgagtcgggtgcaacatctccacattg9gc 62
Qy 315 TGCACAAATGATTACGACTTTGAGGACAGCTGTGGCTCGAGGACGACGAGCTGAG 374
Db 63 tcagaaatgttcaatgactttgacggtaccctgttgctgatgaaacgacagactgaa 122
Qy 375 TAAATCTTCCCTCTGCTCTGCTTTGCAATCTGACTACATTTGAGGCGCTGCTGGAAGA 434
Db 123 caagatattctctggaacttctgaaactgactctgactccatctgagccagtcgacaagca 182
Qy 435 TGAACACAGAGAGCTCTATGCTGAAGCTTCTTCGATCTCTTTTCACTCTATTTGAGTC 494
Db 183 cgagactcagaagagttcagtcctgaagctgtccacatttcttccgtctgattgaatc 242
Qy 495 CTGGGAGTTCCCAAGCAGCTGCTGAGCGGAACCGTCTCAAAACAGCCTGACCGTAGGGAA 554
Db 243 ctgggaggtaccctagccagaccctg-----atcatctccacagcctcaatggtcagaa 296
Qy 555 CCCCACACAGCTACTGAGAGCTGGCCGACTTGAAAATGGGCATCAGTGTGCTCATCCA 614
Db 297 cgcaaccagatctctgagaagctcagcgacctcaagtggtgcatcaacctgctcatcac 356
Qy 615 GGCATGCTCGATGCTCAACCAACATGATGATACGACTCTCTGCGCGCTG---CCTTT 671
Db 357 ggggagccaggtggtgactgagctggtgatgacaatgactctcagcagctgccccctta 416
Qy 672 TGAGGACTTCTACTTGACCATGGGGAGAAC---AACCTCAGAGAGAGCTTTGCTGCTGCT 728
Db 417 cgggaactactaccagaacctgggggagcagcgaacgtcagaggaaactacgagttgtt 476
Qy 729 GCGTTGCTTCAAGAGGACATGCACAAAGTCGAGACCTACTTGAGGGTTGCAAAATTCGAG 788
Db 477 ggcattctcaagaaggacatgcacaaggtcagacctactctgacctgacgctcgaagtgcag 536
Qy 789 GAGATCCCTGGATCCAACTGCACCCCTGTAG 816
Db 537 gaagtcactggaggccaactgcactctg 564

RESULT 10

Q29359
ID Q29359 standard; cDNA; 1119 BP.
XX
XX Q29359;
XX
XX 08-MAR-1993 (first entry)
DT
XX
XX Salmon growth hormone gene.
DE GH; transgenic; fish; antifreeze protein promoter; ss.
KW
XX
XX Oncorhynchus keta.
OS
XX
XX Key Location/Qualifiers
FT 6..638
FT CDS /*tag= a
FT


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Db 363 cgcacacagatctctgagaagctcagacacctcaaaagtgagcatcaacactgctcatcac 422
QY 615 GGCATGCTCGATGCTCAACAAACATGGATGATAAAGACCTCTTGGCGGTG---CCTTT 671
Db 423 gggagcagagatgagctactaagcctggatgacaaagctcagcagctgcccccccta 482
QY 672 TGAGGACTTCTACTGTGACCATGGGGGAGAAC---AACCTCAGAGAGAGCTTTCTGCTGCT 728
Db 483 cgggaactactaccagaacctggggggcgagcggaaacgtcagggaggaactacagattgtt 542
QY 729 GGCCTGCTTCAAGAGAGACATGCACAAAGTCGAGACCTACTGTGAGGGTTGCAAAATTCGAG 788
Db 543 ggcattgctcaagaagtacatgcacaaggtcagacacctactgaccgcgcgaagtgcag 602
QY 789 GAGATCCCTGGATTCCAACTGCACCCCTGTAG 819
Db 603 gaagtactctggaggccaaactgcactctgtag 633

RESULT 12
Q06131
ID Q06131 standard; DNA; 633 BP.
AC Q06131;
XX
XX
XX 05-FEB-1991 (first entry)
XX
XX Sequence encoding rainbow trout Growth hormone GH1.
XX
XX Fish growth hormone; salmon; FGH; SGH; ds.
XX
XX Salmo gairdneri.
XX
XX JP02243700-A.
XX
XX 27-SEP-1990.
XX
XX 17-MAR-1989; 89JP-0063594.
XX
XX 17-MAR-1989; 89JP-0063594.
XX
XX (NIUS ) NIPPON SUISAN KAISHA.
XX
XX WPI; 1990-338513/45.
XX
XX P-PSDB; R07642.
XX
XX Growth hormone gene of fish - contains polypeptide with specific
XX aminoacid sequence
XX
XX PS Disclosure; Fig 1; 8pp; Japanese.
XX
XX Fish growth hormone may be used to accelerate growth in cultured
XX fish.
XX
XX Sequence 633 BP; 163 A; 174 C; 158 G; 138 T; 0 other;
XX

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Query Match 33.0%; Score 270.6; DB 11; Length 633;
Best Local Similarity 70.9%; Pred. No. 9e-68;
Matches 405; Conservative 0; Mismatches 154; Indels 12; Gaps 3;

QY 255 AGACACACAGCGCTCTTCAATATGCAGTCATTCGTGTACACACCTGCACGACGTGGC 314
Db 69 agaaacacacgctctcaactcgcggtcagcccgctgcaacatctccacctattggc 128
QY 315 TGCAAAATGATTAAACGATTTTGAGGACAGCCTGTCCTTGAGGAACGACAGAGCTGAG 374
Db 129 tcagaaaatttcaatgactattgacgggtaccctgtgtcctgtagaacgcagacagcggaa 188
QY 375 TAAATCTTCCCTCTGCTTCTGCAATTCGTACTACATTCGAGCGGCTGCTGGAAGAAGA 434
Db 189 caagatatctcgtggaactctgttaactctgactcactcgtgagcccgctgcaagaaga 248

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```

QY 435 TGAACACAGAGAGAGCTCTATGCTGAAGCTTCTTGCATCTCTTTTCACTCATTTGAGTC 494
Db 249 cgagactcagaagagttcagctcagctgaagctgtccatatactcttccgctgattgaatc 308
QY 495 CTGGAGGTTCCCAACCCAGTCCCTGAGCGGAAACCGGCTCAACACAGAGCTGACCGTAGGGAA 554
Db 309 ctgggagTaccctagccagaccctg-----atcattcccaacagcctaattggtcagaaa 362
QY 555 CCCCAACAGCTCACTGAGAGCTGGCCGACCTGAAATGGGCATCAGTCTGCTCATCCCA 614
Db 363 tgcacaacagatctctgagaagctcagcgacctcaaaagtgagcactcaactgctcatcac 422
QY 615 GGCATGCTCGATGCTCAACCAACATGGATGATAAAGACCTCTTGGCGGTG---CCTTT 671
Db 423 ggggagcagagatgagctactgagcctggatgacaaagctcagcagctgcccccccta 482
QY 672 TGAGGACTTCTACTGTGACCATGGGGGAGAAC---AACCTCAGAGAGAGCTTTGCTGCTGCT 728
Db 483 cgggaactactaccagaacctggggggcgagcggaaacgtcagggaggaactacagattgtt 542
QY 729 GGCCTGCTTCAAGAGAGACATGCACAAAGTCGAGACCTACTTGCAGGGTTGCAAAATTCGAG 788
Db 543 ggcattgctcaagaagtacatgcacaaggtcagacacctactgaccgcgcgaagtgcag 602
QY 789 GAGATCCCTGGATTCCAACTGCACCCCTGTAG 819
Db 603 gaagtactctggaggccaaactgcactctgtag 633

RESULT 13
Q10874
ID Q10874 standard; DNA; 555 BP.
AC Q10874;
XX
XX 13-MAY-1991 (first entry)
XX
XX Plasmid pMWTFWL contg. motilin-encoding DNA as a fusion gene.
XX
XX Motilin; fusion protein; white salmon growth hormone; gamma IFN;
XX beta galactosidase; ss.
XX
XX Key Location/Qualifiers
XX CDS 1..555
XX FT /*tag= a
XX FT misc_RNA 1..489
XX FT /*tag= b
XX FT /*product= white salmon growth hormone peptide
XX FT misc_RNA 490..555
XX FT /*tag= c
XX FT /*product= motilin polypeptide
XX
XX JP03027294-A.
XX
XX 05-FEB-1991.
XX
XX 23-JUN-1989; 89JP-0162020.
XX
XX 23-JUN-1989; 89JP-0162020.
XX
XX (KYOW ) KYOWA HAKKO KOGYO KK.
XX
XX WPI; 1991-078672/11.
XX
XX P-PSDB; R10979.
XX
XX Fused polypeptide for activating motion of intestines -
XX comprising motilin or its derivs. and peptide of specified m.wt.
XX
XX Disclosure; page 5; 17pp; Japanese.
XX
XX This sequence, of plasmid pMWTFWL, comprises a motilin polypeptide
XX -encoding sequence fused to a white salmon growth hormone (wSGH)

```


ID N81504 standard; DNA; 630 BP.
XX AC N81504;
XX DT 14-SEP-1990 (first entry)
XX DE cDNA encoding GH-1.
XX KW GH-1; immunoglobulin-G agglutination activity.
XX FH Key Location/Qualifiers
XX FT CDS 1..630
XX FT /*tag= a
XX PN JP63214195-A.
XX PD 06-SEP-1988.
XX PF 28-FEB-1987; 87JP-0046595.
XX PR 28-FEB-1987; 87JP-0046595.
XX PA (KYOM) KYOWA HAKKO KOGYO KK.
XX WPI; 1988-290584/41.
XX P-PSDB; P81165.
XX Novel proteins and DNA sequences coding for them -
XX PT having immunoglobulin-G agglutination activity
XX PS Disclosure; Page 610; 30pp; Japanese.
XX CC The patent claims a protein having sequence 1, 13 or 15, and IgG
XX CC agglutination activity, DNA having nucleotide sequence encoding proteins
XX CC of sequences 1, 13 and 15, recombinant DNA comprising integrated DNA
XX CC encoding proteins of sequences 1, 13 and 15, and microorganisms
XX CC containing the recombinant DNA.
XX SQ Sequence 630 BP; 161 A; 168 C; 159 G; 142 T; 0 other;

Search completed: May 16, 2001, 10:06:21
Job time: 2614 sec

Query Match 24.8%; Score 203.2; DB 9; Length 630;
Best Local Similarity 61.8%; Pred. No. 1.6e-48;
Matches 341; Conservative 0; Mismatches 208; Indels 3; Gaps 1;
QY 268 CRCTTCATATATGACGCTTCTGTACACACCTGCACGAGCTGGCTGCAAAATGATT 327
DB 82 ctcttcaccagcgctgttaaccgagcacagcacctgcacacactggtcggaatatatc 141
QY 328 AACGACTTTGAGGACAGCCTGTGCTGAGGACGAGCAGCTGAGTAAATCTCCCT 387
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QY 388 CTGCTCTTCTGCAATCTGACTACATTGAGCGCCTGCTGAAAAGATGAACACAGAAG 447
DB 202 ttggccgggtgttactccgactccatccctaccacagggcaagatgaacgcagggag 261
QY 448 AGCTCTATGCTGAAGCTTCTTCGCTATCTCTTTACCTCATTTGAGTCTGGGAGTTCCCA 507
DB 262 aaatcgatgggtactgtctgcacatctctcagccctgacccagtcagtggtgtatcct 321
QY 508 AGCCAGTCCCTGAGCGGAACCGTCTCAACAGCCTGACCGTAGGGAACCCCAACCGCTC 567
DB 322 ctgaagacctgagcgatgctttctctaacagcctgatgtttgggacctctgatgggatac 381
QY 568 ACTGAGAAGCTGGCCGACTGAAATGGGCATCAGTGTGCTCATCCAGGCATGCTCGAT 627
DB 382 ttgtataagctgagggacatgaacagggcatcaatgaattaggtttaggtgac 441
QY 628 GGTCAACCAACATGGATGATACGACTCCTTCCGCTGCTTTTGGAGGACTTCTACTTG 687
DB 442 ggtgattattagggatgtgagaaatctcccggtacgagaacttcgacgtacacct- 500

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 16, 2001, 09:01:02 ; Search time 67.34 seconds
(without alignments)
2123.546 Million cell updates/sec

Title: US-09-402-488A-3

Perfect score: 819

Sequence: 1 ATCGGGGTTCTCATCATCA.....ATTCCAACTGCACCCCTGTAG 819

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0.

Searched: 302621 seqs, 87301344 residues

Total number of hits satisfying chosen parameters: 605242

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents_NA.*

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- 2: /cgn2.6/ptodata/1/ina/5B_COMB.seq.*
- 3: /cgn2.6/ptodata/1/ina/6A_COMB.seq.*
- 4: /cgn2.6/ptodata/1/ina/6B_COMB.seq.*
- 5: /cgn2.6/ptodata/1/ina/PCTUS_COMB.seq.*
- 6: /cgn2.6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES										
Result No.	Score	Query Match	Length	DB ID	Description					
1	278.6	34.0	1201	1	US-08-286-872-1	Sequence 1, Appl				
2	157.2	19.2	576	1	US-08-093-383-4	Sequence 4, Appl				
3	152.4	18.6	601	1	US-07-764-655D-6	Sequence 6, Appl				
4	152.4	18.6	601	1	US-07-801-164A-3	Sequence 3, Appl				
5	152.4	18.6	603	1	US-07-764-655D-7	Sequence 7, Appl				
6	150.8	18.4	576	1	US-07-885-689A-28	Sequence 28, Appl				
7	150.8	18.4	579	1	US-07-885-689A-36	Sequence 36, Appl				
8	150.8	18.4	579	1	US-07-885-689A-37	Sequence 37, Appl				
9	147.2	18.0	755	1	US-08-468-824-5	Sequence 5, Appl				
10	146.8	17.9	600	6	5514646-37	Patent No. 5514646				
11	142.8	17.4	633	1	US-08-388-267C-1	Sequence 1, Appl				
12	140.4	17.1	573	5	PCT-US93-09232-1	Sequence 1, Appl				
13	140.4	17.1	579	1	US-07-621-197C-1	Sequence 1, Appl				
14	140.4	17.1	579	1	US-08-363-982-1	Sequence 1, Appl				
15	138.8	16.9	573	1	US-07-963-331D-1	Sequence 1, Appl				
16	135.6	16.6	570	1	US-07-963-331D-2	Sequence 2, Appl				
17	127.2	15.5	1240	1	US-08-240-372-2	Sequence 2, Appl				
18	126.2	15.4	2732	6	5217891-14	Patent No. 5217891				
19	126.2	15.4	2733	2	US-08-846-021A-6	Sequence 6, Appl				
20	115	14.0	153	2	US-08-679-865-41	Sequence 41, Appl				
21	115	14.0	153	2	US-08-680-876-41	Sequence 41, Appl				
22	115	14.0	1056	1	US-08-457-245-20	Sequence 20, Appl				
23	115	14.0	1056	2	US-08-701-191A-5	Sequence 5, Appl				
24	98.8	12.1	105	2	US-08-687-865A-23	Sequence 23, Appl				
25	98.4	12.0	234	2	US-08-687-865A-20	Sequence 20, Appl				
26	98	12.0	129	2	US-08-679-865-38	Sequence 38, Appl				
27	98	12.0	129	2	US-08-680-876-38	Sequence 38, Appl				

28 96.8 11.8 2081 2 US-09-096-982-7 Sequence 7, Appl
29 96.8 11.8 2081 3 US-08-653-650A-7 Sequence 7, Appl
30 96.2 11.7 1599 3 US-08-737-336-5 Sequence 5, Appl
31 96 11.7 96 3 US-08-737-336-2 Sequence 2, Appl
32 93.4 11.4 762 4 US-09-004-731-91 Sequence 91, Appl
33 93.4 11.4 762 4 US-08-749-699-91 Sequence 91, Appl
34 93.4 11.4 811 4 US-09-004-731-88 Sequence 88, Appl
35 93.4 11.4 811 4 US-08-749-699-88 Sequence 88, Appl
36 91.8 11.2 783 4 US-09-004-731-93 Sequence 93, Appl
37 91.8 11.2 783 4 US-08-749-699-93 Sequence 93, Appl
38 91.8 11.2 823 4 US-09-004-731-90 Sequence 90, Appl
39 91.8 11.2 823 4 US-08-749-699-90 Sequence 90, Appl
40 90.4 11.0 3872 2 US-08-331-081B-4 Sequence 4, Appl
41 87.4 10.7 1896 1 US-08-605-541B-11 Sequence 11, Appl
42 83 10.1 838 1 US-08-318-193-13 Sequence 13, Appl
43 83 10.1 846 6 5200327-5 Patent No. 5200327
44 82.8 10.1 596 1 US-07-826-928A-29 Sequence 29, Appl
45 82.2 10.0 579 1 US-08-093-383-2 Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-08-286-872-1
; Sequence 1, Application US/08286872
; Patent No. 5675061
; GENERAL INFORMATION:
; APPLICANT: Powers, Dennis A.
; TITLE OF INVENTION: Isolation and Characterization
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: P.O. Box 60850
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306-0850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/286,872
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/192,272
; FILING DATE: 04-FEB-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Fabian, Gary R.
; REGISTRATION NUMBER: 33,875
; REFERENCE/DOCKET NUMBER: 8600-0144.30
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1201 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: Coho Salmon Growth Hormone Gene
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 65..697
; OTHER INFORMATION: /note= "Growth Hormone Precursor"
; FEATURE:

NAME/KEY: sig_peptide
LOCATION: 65..130
OTHER INFORMATION: /note= "growth hormone signal"
OTHER INFORMATION: peptide

FEATURE:
NAME/KEY: mat_peptide
LOCATION: 131..697
OTHER INFORMATION: /note= "Growth Hormone"
US-08-286-872-1

Query Match 34.08; Score 278.6; DB 1; Length 1201;
Best Local Similarity 71.8%; Pred. No. 5.6e-76;
Matches 410; Conservative 0; Mismatches 149; Indels 12; Gaps 3;

QY 255 AGACAAACAGCGGCTCTTCATATGATGAGTATGCTGATACAAACCTGCACCACTGGC 314
DB 133 AGAAACCAACGGCTCTTCAACATCGCGGTGAGTGGTGAACATCTCCACCTATTGGC 192
QY 315 TGCAAAATGATTACGACTTTGAGGACAGCTGTGCTGAGGAACGACAGCTGAG 374
DB 193 TCAGAAATGTTCAATGACTTTGAGGTATCCCTGTGCTGATGAACGACAGCTGAA 252
QY 375 TAAATCTTCCCTCTGCTTCTTCAATTCAGTATGCTGCTGAGGCGCTGCTGGAAGA 434
DB 253 CAAGATATCTCTGGACTTCTGTAACCTGACTCCATCTGAGCCGAGTCGACAAGCA 312
QY 435 TGAACACAGAGAGCTATGCTGAGACTTCTTCCGATCTCTTTTACACCTATTGAGTC 494
DB 313 CGAGACTCAGAAGAGTTTCAGTCTCCTGAGCTGCTCCATATTTCTTCCGCTGATTGAATC 372
QY 495 CTGGGAGTCCCAAGCAGCTCCCTGAGCGAAGCTCTCAACAGCCTGACCGTAGGAA 554
DB 373 CTGGGAGTACCTGACAGACCCCTG-----ATCATCTCCACAGCCTATTGGTCGGA 426
QY 555 CCCCAACAGCTCACTGAGAGCTGGCGAGCTTGAATGGGCATCAGTGTGCTCATCCA 614
DB 427 CGCAACACAGATCTCTGAGAAGCTCAGGAGCTCAAGTGGGCATCAACCTGCTCATCAT 486
QY 615 GGCATGCTCATGGTCAACCAACATGGATGATGAACAGCTCTTGGCGCTGCC---TTT 671
DB 487 GGGAGCAGCAGATGGCTTACTGAGCTGGATGACAAATGACTCTCAGCAGCTGCCCGCTA 546
QY 672 TGAGGACTTCTACTTGACCTGGGGGAGAAC---AACCTCAGAGAGAGCTTTTCGCTGCT 728
DB 547 CGGAACACTACTACAGAACCCGGGGGGGCGAGGAACGTCAGGAGAACTACGAGTTGTT 606
QY 729 GGCTTGCTTCAAGAGGACATGCACAAAGTCGAGACCTTACTTTGAGGGTTGCAAAATTGCAG 788
DB 607 GGCTTGCTTCAAGAGGACATGCACAAGGTCGAGACCTTACCTGACCGTCGCAAGTGCAG 666
QY 789 GAGATCCCTGGATTCCTCACTGCACCTCTGAG 819
DB 667 GAAGTCACTGGAGGCCAACTGCACCTCTGAG 697

RESULT 2
US-08-093-383-4
Sequence 4, Application US/08093383
Patent No. 5489529
GENERAL INFORMATION:
APPLICANT: DeBoer, Herman A.
APPLICANT: Heyneker, Herbert L.
APPLICANT: Seeburg, Peter H.
TITLE OF INVENTION: DNA for Expression of Bovine Growth Hormone
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/093.383
FILING DATE: 14-JUL-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/619827
FILING DATE: 28-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/198824
FILING DATE: 05-APR-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 06/632361
FILING DATE: 19-JUL-1984
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 06/303687
FILING DATE: 18-SEP-1981
ATTORNEY/AGENT INFORMATION:
NAME: Johnston, Sean A.
REGISTRATION NUMBER: P35,910
REFERENCE/DOCKET NUMBER: 46C4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-3562
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 576 bases
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-093-383-4

Query Match 19.28; Score 157.2; DB 1; Length 576;
Best Local Similarity 56.5%; Pred. No. 6.9e-39;
Matches 313; Conservative 0; Mismatches 238; Indels 3; Gaps 1;
QY 266 GCCTCTTCAATATGACGATTCGTGTACAAACACCTGCACAGCTGGCTGCAAAATGA 325
DB 26 GTCATTCTCGCTAACGCTGTCTTCGTGCTCAGCATCTTTCATCAGCTGGCTGACACCT 85
QY 326 TTAACGACTTTGAGGACAGCTGTTCGCTGAGGAAGCAGACAGCTGAGTAAATCTTCC 385
DB 86 TCAAAAGAGTTTGAGCGCACCTACATCCCGAGGGACAGAGATACCTCATCCAGAACACC 145
QY 386 CTCGTCTTCTTGCATTTCTGACTACATTTGAGGCGCTGCTGAAAGATGAACACAGA 445
DB 146 AGGTTCGCTTCTGCTTCTGAAACCATCCCGCCCCCAGGCAAGGATGAGGCCAGC 205
QY 446 AGAGCTCTATGCTGAAGCTTCTTCGCTATCTCTTTTCACTTCATTTGAGTCTGGAGTTCC 505
DB 206 AGAATCAGACTTGGAGCTGCTTCGCTATCTCTCTCTCATCTCAGTCTGGCTGGGC 265
QY 506 CAAGCCAGTCTCTGAGCGGAACCGTCTCAACAGCTGACCGTGAAGAACCCCAACAGC 565
DB 266 CCCTGCAGTTCTCTCAGCAGAGTCTTCCACCAACAGCTTGTGTTTGGCACCTCGGCGTG 325
QY 566 TCAGTGAAGAGTGGCCGACTTGAATATGGGATCATGCTGCTCATCCAGGCACTGCTCG 625
DB 326 TCATGAGAAGCTGAAGGACCTGGAGGAAGCATCTCTGCGCTGATGCGGAGCTGGAAG 385
QY 626 ATGGTCAACCAACATGATGATTAACGACTCTCTTTCGCTGCTCTTTTGGAGCACTTCTACT 685
DB 386 ATGGACCCCGGGGCTGGGAGATCTCTCAAGCAGACCTATGACAAATTTGACACAAACA 445
QY 686 TGACCATGGGGAGAACACCTCAGAGAGAGCTTTCGCTGCTGCTGCTTGTTCGAAGAAG 745
DB 446 TCGGCA---GTACGACGCGGCTGCTCAAGACTACCGTCTGCTCTCTCTCTCGGAGG 502

Matches 310; Conservative 0; Mismatches 241; Indels 3; Gaps 1;

QY 266 GGCTCTTCAATAATGACGATTCATGTCACACACCTGCACGAGCTGGCTGCAAAATGA 325
DB 51 GCCTGTTTCCCAACGCTGTGCTCCGGGCTCAGCAGCTGCATGCTGTGTGACACCT 110
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DB 171 AGTTTGCTCTTCTGCTTCTGAAACATCCCGGCCCCACGGGCAAGATGAGGCCAGC 230
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DB 231 AGAAATCAGACTTGAGGCTGTCTGCACTCTCACTGCTCTCATCCAGTCTGGTGGGC 290
QY 506 CAAGCCAGTCCCTGAGCGGAACCGTCTCAACAGAGCTGACCGTAGGGAACCCCAACAGC 565
DB 291 CCTCGAGTCTCTCAGCAGAGCTTTCACCAACAGCTTGTGTGTCACCTCGGACCGTG 350
QY 566 TCAGTGAAGCTGCGCGACTTGAATGGGATCAGTGTGTCATCCAGGAGTCTCTCG 625
DB 351 TCTATGAGAAGCTGAAGACCTGGAGGAGGATCTCTGCGCTGTGTCGGGAGTGGAG 410
QY 626 ATGGTCAACCAACATGATGATAGGACTCTCTGCGGCTGCTTTGAGGACTTCTACT 585
DB 411 ATGGCACCCCGGCTGGGAGAGTCTCTCAAGCAGACCTATGACAAATTTGACACAAACA 470
QY 686 TGACCATGGGAGAGAACACCTCAGAGAGAGCTTCTGCTGCTGCTGCTTCAAGAAGG 745
DB 471 TCGCA---GTGACAGCGCTGCTCAAGAACTACGGTCTGCTCTCTCGTCCGGAAG 527
QY 746 ACATGCACAAAGTCGAGACTACTTGAAGGTTGCAAAATTCAGGAGATCCCTGGATTCCA 805
DB 528 ACCTGCATAAGACGAGAGCTACCTGAGGTCATGAAGTGCCCGCCCTTCGGGAGGCCA 587
QY 806 ACTGCACCTGTAG 819
DB 588 GCTGTGCTTCTAG 601

RESULT 5
US-07-764-655D-7/c
; Sequence 7, Application US/07764655D
; Patent No. 5378613
; GENERAL INFORMATION:
; APPLICANT: BELAGAJE, RAMA M.
; TITLE OF INVENTION: INCREASED EXPRESSION OF LOW MOLECULAR
; WEIGHT RECOMBINANT POLYPEPTIDES.
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PAUL CANTRELL 1116
; STREET: LILLY CORPORATE CENTER
; CITY: INDIANAPOLIS
; STATE: IN
; COUNTRY: USA
; ZIP: 46285
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: Macintosh 5.0
; SOFTWARE: Microsoft Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07764,655D
; FILING DATE: 19910924
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: JONES, JOSEPH A
; REGISTRATION NUMBER: 26,472
; REFERENCE/DOCKET NUMBER: X8031
; TELECOMMUNICATION INFORMATION:

TELEPHONE: 317-276-3885
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 603 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-07-764-655D-7

Query Match 18.6%; Score 152.4; DB 1; Length 603;
Best Local Similarity 56.0%; Pred. No. 2.1e-37;
Matches 310; Conservative 0; Mismatches 241; Indels 3; Gaps 1;

QY 266 GGCTCTTCAATAATGACGATTCATGTCACACACCTGCACGAGCTGGCTGCAAAATGA 325
DB 555 GCCTGTTTCCCAACGCTGTGCTCCGGGCTCAGCAGCTGCATGCTGTGTGACACCT 496
QY 326 TTAACGACTTTGAGGACGAGCTGTGCTCCGAGGACGACGAGCTGAGTAAATCTTCC 385
DB 495 TCAAGAGTTTGAGCGCACTATACCCGAGGACAGAGATCTCCATCCAGAACACC 436
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DB 315 CCTGAGACTTCTCAGCAGAGTCTTCAACACAGCTTGTGTGTCACCTCGGACCGTG 256
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DB 135 TCGCA---GTGACAGCGCTGCTCAAGAACTACGGTCTGCTCTCTCTCTCGGAGG 79
QY 746 ACATGCACAAAGTCGAGACTACTTGAAGGTTGCAAAATTCAGGAGATCCCTGGATTCCA 805
DB 78 ACCTGCATAAGACGAGAGAGCTACCTGAGGTCATGAAGTGCCTTCGGGAGGCCA 19
QY 806 ACTGCACCTGTAG 819
DB 18 GCTGTGCTTCTAG 5

RESULT 6
US-07-885-689A-28
; Sequence 28, Application US/07885689A
; Patent No. 5365876
; GENERAL INFORMATION:
; APPLICANT: Cho, Joong M.
; APPLICANT: Lee, Tae H.
; APPLICANT: Chung, Hyun H.
; APPLICANT: Lee, Yong B.
; APPLICANT: Lee, Tae G.
; APPLICANT: Park, Young W.
; APPLICANT: Han, Kyu B.
; TITLE OF INVENTION: Method for Production of Bovine Growth
; HORMONE USING A SYNTHETIC GENE.
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Birch, Stewart, Kolash & Birch

STREET: P.O. Box 747
CITY: Falls Church
STATE: Virginia
COUNTRY: USA
ZIP: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/885,689A
FILING DATE: 19-MAY-1992
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Svensson, Leonard R.
REGISTRATION NUMBER: 30,330
REFERENCE/DOCKET NUMBER: 377-144P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-241-1300
TELEFAX: 703-241-2848
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 576 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ORIGINAL SOURCE: Bovine
FEATURE:
NAME/KEY: CDS
LOCATION: 1..573
OTHER INFORMATION: /product= "Bovine growth hormone"
US-07-885-689A-28

Query Match 18.4%; Score 150.8; DB 1; Length 576;
Best Local Similarity 55.8%; Pred. No. 6.3e-37;
Matches 309; Conservative 0; Mismatches 242; Indels 3; Gaps 1;

QY 266 GCCTCTTCAATATGACGATTCCTGTTACAAACCTGCACACCTGGCTGCAAAAATGA 325
DB 26 GTCATTCGCTAAACGCTGTTCTCGAGCTCAGCATCTTCATCAGCTGGCTGCACACCT 85
QY 326 TTAACGACCTTTAGACACACCTGTTCCCTGAGGAGGACGACGCTGAGTAAATCTTC 385
DB 86 TCAAAGAGTTTGAGCGCACCTACATCCCGAGGAGGACAGATACCTCCAGAACACCC 145
QY 386 CTCCTGCTTCTGCAATTCGTACTATGAGCGGCTGCTGAAAGATGAACACAGA 445
DB 146 AGGTGCTCTGCTCTCTGAAACATCCCGCCCGCCAGCAAGATGAGCCACG 205
QY 446 AGAGCTCTATGCTGAAGCTTCTTCGATCTCTTTTACCTCATTTGAGTCTCTGGAGTTCC 505
DB 206 AGAATACAGACTTGAGCTGCTTGCATCTCTGCTGATCCAGCTGCTGCTCGGC 265
QY 506 CAAGCCAGCTCCTGAGCGAACCTCTCAACAGCCTGACCGTAGGGAACCCCAACAGC 565
DB 266 CCCTGAGCTTCTCAGAGAGCTTTCACCAACAGCTTGTGTGTTGAGCTCGGACCGTG 325
QY 566 TCACGTGAAGCTGCCGACTTGAATATGGGATCAGTGTGCTCATCCAGGATGCTCTCG 625
DB 326 TCTATGAGAGCTGAAGATCTAGAGGAGGATCTTGGCCCTGATGCGGGAGCTGGAG 385
QY 626 ATGCTCAACCAACATGATGATGAACGACTCTCTGCGCTGCTTTTGGAGACTTCTACT 685
DB 386 ATGGCACCCCGGCTGGGAGATCTCTCAACGACCTATGACAAATTTGACACAAACA 445
QY 686 TGACCATGGGAGAACACCTCAGAGAGAGCTTTCGCTGTGCTGCTGCTTCAAGAAGG 745
DB 446 TCGCGA---GTGACGACGCGTGTCTCAAGAACTACGGTCTGCTCTCTCTCTCTCGGAGG 502

QY 746 ACATGCACAAATCGAGACCTACTTGAGGTTGCAAAATTCAGGAGATCCCTGGATTCCA 805
DB 503 ACCTGCATAGACGAGACGTACCTGAGGGTCATGAAGTGCCTTCGGGGAGGCCA 562
QY 806 ACTGCACCCCTGTAG 819
DB 563 GCTGCGCTTCTAG 576

RESULT 7
US-07-885-689A-36
Sequence 36, Application US/07885689A
Patent No. 5366876
GENERAL INFORMATION:
APPLICANT: Cho, Joong M.
APPLICANT: Lee, Tae H.
APPLICANT: Chung, Hyun H.
APPLICANT: Lee, Yong B.
APPLICANT: Lee, Tae G.
APPLICANT: Park, Young W.
APPLICANT: Han, Kyu B.
TITLE OF INVENTION: Method for Production of Bovine Growth
TITLE OF INVENTION: Hormone Using a Synthetic Gene.
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Birch, Stewart, Kolash & Birch
STREET: P.O. Box 747
CITY: Falls Church
STATE: Virginia
COUNTRY: USA
ZIP: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/885,689A
FILING DATE: 19-MAY-1992
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Svensson, Leonard R.
REGISTRATION NUMBER: 30,330
REFERENCE/DOCKET NUMBER: 377-144P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-241-1300
TELEFAX: 703-241-2848
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 579 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: /label= 5'end
LOCATION: 1..60
OTHER INFORMATION: /note= "5' proximal sequence of BGH insert in
OTHER INFORMATION: ptrphsBGH1-13, shown in Fig...."
US-07-885-689A-36

Query Match 18.4%; Score 150.8; DB 1; Length 579;
Best Local Similarity 55.8%; Pred. No. 6.4e-37;
Matches 309; Conservative 0; Mismatches 242; Indels 3; Gaps 1;

QY 266 GCCTCTTCAATATGACGATTCCTGTTACAAACCTGCACACCTGGCTGCAAAAATGA 325
DB 29 GTCATTCGCTAAACGCTGTTCTTCGAGCTCAGCATCTTCATCAGCTGGCTGCTGACACCT 88

NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: SPENCER, FRANK & SCHNEIDER
STREET: 1111 Nineteenth St., N.W.,
CITY: Washington
STATE: DC
COUNTRY: US
ZIP: 20036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,824

[illegible]

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RESULT 10
5514646-37
; Patent No. 5514646
; APPLICANT: CHANCE, RONALD E.; DIMARCHI, RICHARD D.; FRANK,
; BRUCE H.; SHIELDS, JAMES E.
; TITLE OF INVENTION: INSULIN ANALOGS MODIFIED AT POSITION
; 29 OF THE B CHAIN
; NUMBER OF SEQUENCES: 52
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/57,201
; FILING DATE: 05-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 686,632
; FILING DATE: 17-APR-1991
; APPLICATION NUMBER: 388,201
; FILING DATE: 04-AUG-1989
; APPLICATION NUMBER: 308,352
; FILING DATE: 09-FEB-1989
; SEQ ID NO: 37:
; LENGTH: 600
5514646-37

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Query Match 17.9%; Score 145.8; DB 6; Length 600;
Best Local Similarity 56.5%; Pred. No. 1.1e-35;
Matches 313; Conservative 0; Mismatches 237; Indels. 4; Gaps 2;

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QY 746 ACATGCACAAAGTCGAGACTTACTTCTGAGGGTGTGCAAAATTCAGAGAGATCCCTGGATCCA 805
Db 509 ACCTGCACAAAGCTGAGACATACCTCGGGTCAATGAAGTGTGCGCCGCTTCTGCGGAGCA 568
QY 806 ACTGCACCT 815
Db 569 GCTGTGCTT 578

RESULT 14

US-08-363-982-1
; Sequence 1, Application US/08363982
; Patent No. 5348068
; GENERAL INFORMATION:
; APPLICANT: Fischer, Meir
; APPLICANT: Lebens, Michael R.
; APPLICANT: Chaleff, Deborah T.
; TITLE OF INVENTION: Somatotropins with Alterations in the
; TITLE OF INVENTION: Alpha-Helix 1 Region, and Combinations with Other
; TITLE OF INVENTION: Mutations
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John P. White, Cooper & Dunham
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/363,982
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/010,405
; FILING DATE: 28 JAN 1993
; APPLICATION NUMBER: US/07/621,656
; FILING DATE: 30-NOV-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 38360/JPW/LSW
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 977-9550
; TELEFAX: (212) 664-0525
; TELEX: 422523 Coop ul
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 579 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..579

US-08-363-982-1

Query Match 17.1%; Score 140.4; DB 1; Length 579;
Best Local Similarity 54.7%; Pred. No. 9.9e-34;
Matches 301; Conservative 0; Mismatches 246; Indels 3; Gaps 1;
QY 266 GCTCTTCAATGATGAGTCATTGTGTCACACACCTGCAGAGCTGGCTGCAAAATGA 325
Db 32 GCCTATTGCCAAGCCGTGCTCGGGGCCAGCACCTGCACCACTGGCTGCGCACCT 91

QY 326 TTAACGACTTTGAGCAGACCTGTTCCTGAGGAACGAGACAGCTGAGTAAATCTTCC 385
Db 92 ACAGGAGTTTGAGCGCCCTACATCCGAGGAGCAGAGGTACTCTTCAGAACGCC 151
QY 386 CTCTGTCTTTCTCAATTTCTGACTACATTTGAGGCGCTTCTGGAAGATGAAACACAGA 445
Db 152 AGCTGCTTCTCTCTCGAGACCATCCCGGCCCCACGCGCAAGACGAGGCCAGC 211
QY 446 AGAGCTCTATGCTGAAGCTTCTTCGCAATCTCTTTTACCTCATTTAGTCTCTGGAGTCC 505
Db 212 AGAGATCGGAGCTGGAGCTGCTGCGCTTCTGCTGCTGCTCATCCAGTCGCTGGGC 271
QY 506 CAAGCCAGTCCCTGAGCGGAACCGTCTCAACACGCTGACCGTAGGGAAACCCCAACACG 565
Db 272 CCGTGCAAGTTCTCAGCAGGGTCTTCAACACACGCTGCTGTTGGCACCTTCAGACCGG 331
QY 566 TCACTGAGAAAGCTGGCGCACTTGAAATGGGCATCAGTGTCTCATCCAGGACATGTCTCG 625
Db 332 TCTACGAGAAAGCTGAAGCACTGGAGGAGGCACTCCAGGCCCTGATCGGGAGCTGGAGG 391
QY 626 ATGCTCAACCAACATGATGATTAACGACTCTTTCGCGCTGCCCTTTTGAGGACATCTACT 685
Db 392 ATGCGACGCCCGGCGAGGACATCTCTCAAGCAAACTTACGACAAATTTGACACAACT 451
QY 686 TGACCATGGGGAGAACAACTCTCAGAGAGAGCTTTCTGCTGCTGCTTCAAGAAAGG 745
Db 452 TGGCA---GTGATGACGCGCTGCTTAAGAACTACGGGCTCTCTCTCTCAAGAAAGG 508
QY 746 ACATGCACAAAGTCGAGACCTTACTTTGAGGGTTGCAAAATTCAGGAGATCCCTGGATTCCA 805
Db 509 ACCTGCACAAAGCTGAGACATACCTCGGGTCAATGAAGTGTGCGCGCTTCTGCGGAGCA 568
QY 806 ACTGCACCT 815
Db 569 GCTGTGCTT 578

RESULT 15

US-07-963-331D-1
; Sequence 1, Application US/07963331D
; Patent No. 5334511
; GENERAL INFORMATION:
; APPLICANT: Harada, Yasuhiro
; APPLICANT: Nakano, Eiichi
; APPLICANT: Tatsumi, Hiroki
; APPLICANT: Umez, Motoaki
; TITLE OF INVENTION: Isolated Mink Growth
; TITLE OF INVENTION: Hormone Genes, No. 5334511el Recombinant DNA And
; TITLE OF INVENTION: Methods For Producing Mink Growth Hormone.
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Limbach & Limbach
; STREET: 2001 Ferry Building
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0.
; SOFTWARE: Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/963,331D
; FILING DATE: 19921016
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Derogits, Michael E.
; REGISTRATION NUMBER: 31,243
; REFERENCE/DOCKET NUMBER: HIRA-00600
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 433-4150

Search completed: May 16, 2001, 10:03:58
Job time: 3776 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: May 16, 2001, 08:31:32 ; Search time 1126.9 seconds
(without alignments)
6349.156 Million cell updates/sec

Title: US-09-402-488A-3
Perfect score: 819
Sequence: 1 ATGGGGGTTCTCATCATCA.....ATTCCAACGCACCCCTGTAG 819

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Gapop 10.0 , Gapext 1.0

Searched: 9623517 seqs, 4368049070 residues

Total number of hits satisfying chosen parameters: 19247034

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	ID	Description
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3	138	16.8	280	18	AI308623
4	128.4	15.7	517	139	BE755987
5	124	15.1	547	118	AW659506
6	124	15.1	547	143	BF077176
7	124	15.1	553	139	BE756195
8	124	15.1	576	118	AW631765
9	123.8	15.1	497	150	BF605397
10	120.6	14.7	477	151	BF65271
11	117.6	14.4	476	140	BE861283
12	117.2	14.3	261	114	AW330514
13	115	14.0	697	107	AU170721
14	115	14.0	773	107	AU167389
15	114.6	14.0	495	118	AW657301
16	114.6	14.0	549	118	AW655562
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Query Match 18.0%; Score 147.2; DB 139; Length 570;
Best Local Similarity 55.7%; Pred. No. 4.6e-31;
Matches 303; Conservative 0; Mismatches 238; Indels 3; Gaps 1;

Library made from pooled tissue from testis, thymus, semitendinosus muscle, longissimus muscle, pancreas, adrenal, and endometrium.

BASE COUNT 110 a 165 c 137 g 105 t

Query Match 15.7%; Score 128.4; DB 139; Length 517;
Best Local Similarity 55.3%; Pred. No. 9.9e-26;
Matches 271; Conservative 0; Mismatches 216; Indels 3; Gaps 1;

Qy 266 GGCTCTTCAATATGACGATTCGTGTACAAACACCTGCACACCTGGCTGCAAAAATGA 325
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Db 150 AGTTTGCCTTCTGCTCTCTGAACCATCCCGGCCCGGCGCAAGATGAGGCCAGC 209
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Db 270 CCCTGAGTCTTCACGACAGAGTCTTCAACACAGCTTGTGTGTCACCTCGGACCGTG 329
Qy 566 TCACGTGAGAAGCTGGCGGACTTTGAAATGGGCGATCATGTGCTCATCCAGGCGATGCTCG 625
Db 330 TCTATGAGAGCTGAGGACCTTGGAGAGGATCTTGGCCCTGATCGCGGAGCTGGAAG 389
Qy 626 ATGGTCAACCAACATGATGATTAACGACTCTTTCGCGCTGCTTTTGGAGACTTCTACT 685
Db 390 ATGGCACCCCGGGCTGGGAGATCTTCAACAGACCTATGACAAATTTGACACAAACA 449
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Qy 746 ACATGCACAA 755
Db 507 ACCTGCATAA 516

RESULT 5
LOCUS AW659506 547 bp mRNA EST 14-JUL-2000
DEFINITION 96738 MARC 1B0V Bos taurus cDNA 5', mRNA sequence.
ACCESSION AW659506
VERSION AW659506.1 GI:7425333
KEYWORDS EST.
SOURCE Bos taurus
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.
1 (bases 1 to 547)
Smith,T.P.L., Casas,E., Stone,R.T., Heaton,M.P., Grosse,W.M.,
Bennett,G.A., Fahrenkrug,S.C., Freking,B.A., Rohrer,G.A., Laegreid
W.W. and Keele,J.W.
Design and use of four pooled tissue normalized cDNA libraries for
EST discovery in cattle
Unpublished (2000)
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov

Single pass sequencing. Bases called and alt.trimmed with phred v0.980904.e. Vector identified by cross_match with the -mnscore 18 and -mismatch 12 options.

PCR Primers
FORWARD: AGGAACACGCTATGACCAT
BACKWARD: GTTTCCCGACGACGACG
Plate: 74 row: B column: 7
Seq primer: ATTAGGTGACACTATAG.

FEATURES
source

1..547
/organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lib="MARC 1B0V"
/tissue_type="pooled"
/lab_host="DH10B"
/note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI;
Library made from pooled tissue from lymph node, ovary,
fat, hypothalamus, and pituitary."

BASE COUNT 101 a 183 c 149 g 114 t
ORIGIN

Query Match 15.1%; Score 124; DB 118; Length 547;
Best Local Similarity 58.8%; Pred. No. 1.8e-24;
Matches 214; Conservative 0; Mismatches 150; Indels 0; Gaps 0;

Qy 266 GGCTCTTCAATATGACGATTCGTGTACAAACACCTGCACACCTGGCTGCAAAAATGA 325
Db 147 GCCTGTTGCCAACGCTGTGCTCGGGCTCAGCACCTGCATCAGCTGGCTGCTGACACCT 206
Qy 326 TTAACGACTTTTGGAGGACGCTGTTGCTGAGGAACGACGACGCTGAGTAAAAATCTTCC 385
Db 207 TCAAGAGTTTGGAGCGACCTATATCCGGAGGAGAGAGATATCTCATCCAGACACCC 266
Qy 386 CTCCTGCTTTCTCAATTCGTACTACATTTGAGGCGCTGCTGGAAGATGAACACACAGA 445
Db 267 AGTTCCTTCTCTCTCTGTAACCATCCCGGCCCGGCAAGATGAGCCCGAGC 326
Qy 446 AGAGCTCTATGTGAGAGCTTCTTCCGATCTCTTTTCACTCATTTGAGTCTCTGGAGTTCC 505
Db 327 AGAAATCAGACTTGGAGCTGCTTCCGATCTCACTGCTCTCTCATCCAGTCTGCTTGGGC 386
Qy 506 CAAGCCAGTCCCTGAGCGGAACCTCTCAACAGCCTGACCGTAGGAACCCCAACACAGC 565
Db 387 CCTGAGTCTTCTCAGCAGAGTCTTCAACACAGCTTGGTGTGGCACCTCGGACCGTG 446
Qy 566 TCACGTGAGAAGCTGGCGGACTTGAAAATGGGCATCAGTGTGCTCATCCAGGATGCTCTCG 625
Db 447 TCTATGAGAAGCTGAAGGACCTGGAGGAAGCATCTCTGGCCCTGATCGGGAGCTGGAAG 506
Qy 626 ATGG 629
Db 507 ATGG 510

RESULT 6
LOCUS BF077176 547 bp mRNA EST 18-OCT-2000
DEFINITION 226992 MARC 2B0V Bos taurus cDNA 5', mRNA sequence.
ACCESSION BF077176
VERSION BF077176.1 GI:10871006
KEYWORDS EST.
SOURCE Bos taurus
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.
1 (bases 1 to 547)
Smith,T.P.L., Casas,E., Stone,R.T., Heaton,M.P., Grosse,W.M.,
Bennett,G.A., Fahrenkrug,S.C., Freking,B.A., Rohrer,G.A., Laegreid
W.W. and Keele,J.W.
Design and use of four pooled tissue normalized cDNA libraries for
EST discovery in cattle

LOCUS AW631765 576 bp mRNA EST 14-JUL-2000
DEFINITION 91039 MARC 1BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION AW631765
VERSION AW631765.1 GI:7388845
KEYWORDS EST.
SOURCE COW.
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.
REFERENCE 1 (bases 1 to 576)
AUTHORS Smith,T.P.L., Casas,E., Stone,R.T., Heaton,M.P., Grosse,W.M.,
Bennett,G.A., Fahrenkrug,S.C., Freking,B.A., Rohrer,G.A., Laegreid
,W.W. and Keele,J.W.
TITLE Design and use of four pooled tissue normalized cDNA libraries for
EST discovery in cattle
JOURNAL Unpublished (2000)
COMMENT Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smithemail.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
PCR Primers
FORWARD: AGGAACAGCTATGACCAT
BACKWARD: GTTTCCTCCAGTCACGCG
Plate: 76 row: L column: 20
Seq primer: ATTAGGTGACACTATAG.
FEATURES
Location/Qualifiers
1..576
/organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lib="MARC 1BOV"
/tissue_type="pooled"
/lab_host="DH10B"
/note="vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI;
Library made from pooled tissue from lymph node, ovary,
fat, hypothalamus, and pituitary."
BASE COUNT 113 a 189 c 155 g 119 t
ORIGIN
Query Match 15.1%; Score 124; DB 118; Length 576;
Best Local Similarity 58.8%; Pred. NO. 1.8e-24;
Matches 214; Conservative 0; Mismatches 150; Indels 0; Gaps 0;
QY 266 GGCTCTTCAATAATCAGTCATTGCTGTACACACCTGCACCGCTGGCTGCAAAATGA 325
DB 147 GCCTGTTGGCCAAACGCTGTGCTCCGGGCTTCAGCACCCTGCATCGCTGGCTGACACCT 206
QY 326 TTAAGGACTTTGAGGACGAGCTGTGCTCCAGGAGCGACGACAGCTGAGTAAATCTTCC 385
DB 207 TCAAGAGTTTGAGCGCCTACATCCCGGAGGAGACAGATACTCCATCCAGAACACCC 266
QY 386 CTCTGCTTTCTGCAATTTGACTACTATGAGCGGCTGCTGGAAAGATGAACACAGA 445
DB 267 AGGTTGCGCTTCTGCTTCTGTAACCATCCCGCCCCAGGCGCAAGATGAGGCCACG 326
QY 446 AGAGCTCTATGCTGAAGCTTCTTCGCATCTCTTTTCACCTCAATGAGTCTCTGGAGTTCC 505
DB 327 AGAATACAGACTTGAGGCTGTCTGCTCATCTCTCTCATCCAGTCTGCTGGCTTGGGC 386
QY 506 CAAGCCAGCTCCCTGAGCGGAACCGCTCAACACAGCTTGACCTAGGACCCCAACCCAGC 565
DB 387 CCTGCACTTCTCTAGCAGAGTCTTACCAACAGAGTTGGTGTGGACCTCGGACCGTG 446
QY 566 TCACTGAGAAGCTGCCGCACTTGAATAATGGGCATCAGTGTGCTCATCCAGGCACTGTCTCG 625
DB 447 TCTATGAGAAGCTGAAGACCTGGAGGAGGATCCTGGCCCTGATGCGGAGCTGGAG 506

QY 626 ATGG 629
DB 507 ATGG 510
RESULT 9
BF605397 497 bp mRNA EST 13-DEC-2000
LOCUS 271754 MARC 3BOV Bos taurus cDNA 5', mRNA sequence.
DEFINITION BF605397
ACCESSION BF605397
VERSION BF605397.1 GI:11704971
KEYWORDS EST.
SOURCE COW.
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.
REFERENCE 1 (bases 1 to 497)
AUTHORS Smith,T.P.L., Casas,E., Stone,R.T., Heaton,M.P., Grosse,W.M.,
Bennett,G.A., Fahrenkrug,S.C., Freking,B.A., Rohrer,G.A., Laegreid
,W.W. and Keele,J.W.
TITLE Design and use of four pooled tissue normalized cDNA libraries for
EST discovery in cattle
JOURNAL Unpublished (2000)
COMMENT Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smithemail.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
PCR Primers
FORWARD: AGGAACAGCTATGACCAT
BACKWARD: GTTTCCTCCAGTCACGCG
Plate: 55 row: E column: 9
Seq primer: ATTAGGTGACACTATAG.
FEATURES
Location/Qualifiers
1..497
/organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lib="MARC 3BOV"
/tissue_type="pooled"
/lab_host="DH10B"
/note="vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI;
Library made from pooled tissue from marrow, alveolar
macrophage, ovary, fetal semitendinosus muscle, and fetal
longissimus muscle."
BASE COUNT 90 a 167 c 134 g 106 t
ORIGIN
Query Match 15.1%; Score 123.8; DB 150; Length 497;
Best Local Similarity 59.5%; Pred. NO. 2e-24;
Matches 209; Conservative 0; Mismatches 142; Indels 0; Gaps 0;
QY 266 GGCTCTTCAATAATCAGTCATTGCTGTACACACCTGCACCGCTGGCTGCAAAATGA 325
DB 142 GCCTGTTGGCCAAACGCTGTGCTCCGGGCTCAGCACCCTGCATCGCTGGCTGACACCT 201
QY 326 TTAACGACTTTGAGGACGAGCTGTGCTGAGGAACGACAGCTGAGTAAATCTTCC 385
DB 202 TCAAGAGTTTGAGCGCACCTACATCCCGGAGGACAGAGATACTCCATCCAGAACACCC 261
QY 386 CTCTGCTTTCTGCAATTTGACTACTATGAGCGGCTGCTGGAAAGATGAACACAGA 445
DB 262 AGTGTGCCCTTCTGCTTCTCTGAAACCATCCCGCCCCAGGCGCAAGATGAGGCCAGC 321
QY 446 AGAGCTCTATGCTGAAGCTTCTTCGCATCTCTTTTCACCTCATTTGAGTCTCTGGAGTTCC 505
DB 322 AGAATACAGACTTGAGGAGCTGCTTCGCATCTCACTGCTCTCCATCCAGCTGCTGGCTGGGC 381

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QY 506 CAAGCAGTCCCTGAGCGGACCGCTCTCAACAGCCTGACCTAGGGAACCCCAACACG 565
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 382 CCCTGAGTTCCTCAGCAGAGCTCTTCCACACAGCTTGCTTGGGCACCTCGACCGTG 441
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 566 TCACTGAGAAGCTGGCGGCACTTGAATAATAGGCACTGCTGCTCATCCAGG 616
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 442 TCTATGAGAAGCTGAAGAGCACTGAGGAGGCACTCCTGGCCCTGATGGGG 492
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 10
LOCUS BF655271 477 bp mRNA EST 20-DEC-2000
DEFINITION 279722 MARC 3BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION BF655271
VERSION BF655271.1 GI:11920403
KEYWORDS EST.
SOURCE cow.
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.
1 (bases 1 to 477)
Smith,T.P.L., Casas,E., Stone,R.T., Heaton,M.P., Grosse,W.M.,
Bennett,G.A., Fahrnkruug,S.C., Freking,B.A., Rohrer,G.A., Laegreid
,W.W. and Keele,J.W.
Design and use of four pooled tissue normalized cDNA libraries for
EST discovery in cattle
Unpublished (2000)
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smithemail.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -mismatch 12 options.
PCR Primers
FORWARD: AGGAACAGCTATGACCAT
BACKWARD: GTTTCCCGACGACGAGC
Plate: 75 row: H column: 11
Seq primer: ATTAGCTGACACTATAG.
Location/Qualifiers
1..477
/organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lib="MARC 3BOV"
/tissue_type="pooled"
/lab_host="DH10B"
/note="vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI;
Library made from pooled tissue from marrow, alveolar
macrophage, ovary, fetal semitendinosus muscle, and fetal
longissimus muscle."
87 a 160 c 127 g 103 t

BASE COUNT
ORIGIN

Query Match 14.7%; Score 120.6; DB 151; Length 477;
Best Local Similarity 60.0%; Pred. No. 1.6e-23;
Matches 201; Conservative 0; Mismatches 134; Indels 0; Gaps 0;

QY 266 GCCTCTTAATAATGAGTATTCGTGTATCAACACCTGCACACGCTGCTGCAGAAATGA 325
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 138 GCCTGTGTCCCAAGCTGTGCTCGGGCTCAGCACCTGCATCAGCTGGCTGCACACCT 197
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 326 TTACGAGCTTTGAGACAGCTGTGCTGTAGGACGAGCAGCTGAGTAAATCTTCC 385
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 198 TCAAGAGTTTTSAGCGCACCTTACATCCCGGAGGACAGAGATACCTCCACAGAACCCC 257
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 386 CTCGTCTTCTTCAATCTCAGTACATTTAGGCGCTGTGGGAAAGATGAACACACAGA 445
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 258 AGGTGCTCTTCTCTCTGAACCACTCCCGGGCCCCCAGGCAAGTAAGAGGCCACG 317
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

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QY 446 AGAGCTCTATGCTGAAGCTTCTTTCGATCTCTTTTACCTCATTCAGTCTGGAGTTCC 505
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 318 AGAANTCAGACTTGAGAGCTGCTTCCGATCTACTGCTCTCATCCAGTCTGCTGGCTGGGC 377
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 506 CAAGCAGTCCCTGAGCGGAAACCGCTCTCAACAGCCTGACCTAGGGAACCCCAACACG 565
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 378 CCCTCAGTTCCTCAGCAGAGCTTTCACCAACAGCTTGGTGTGGTGGCACCTGGGACCGTG 437
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 566 TCACTGAGAAGCTGGCGGCACTTGAATAATGGGCATC 600
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 438 TCTATGAGAAGCTGAAGGACCTGGAGGAGGCATC 472
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 11
LOCUS BE861283 476 bp mRNA EST 29-SEP-2000
DEFINITION UI-M-AJ1-ahh-h-03-0-UI.r1 NIH_BMAP_MOB_N Mus musculus cDNA clone
UI-M-AJ1-ahh-h-03-0-UI 5', mRNA sequence.
ACCESSION BE861283
VERSION BE861283.1 GI:10379077
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 476)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
discovery
Genome Res. 6 (9), 791-806 (1996)
97044477
Contact: Chin, H
National Institute of Mental Health
6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
20892-9643, USA
Tel: 301 443 1706
Fax: 301 443 9890
Email: mEST@mail.nih.gov
cDNA Library Preparation: M.B. Soares Lab Clone distribution:
Researchers may obtain BMAP cDNA clones from RESEARCH GENETICS. It
should be noted that Bento Soares is generating a small number of
additional specialized non-redundant arrays of BMAP cDNAs whose
availability will be considered under appropriate and limited
collaborative arrangements
Seq primer: M13 Reverse.
Location/Qualifiers
1..476
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone_lib="NIH_BMAP_MOB_N"
/dev_stage="27-32 days"
/lab_host="DH10B (Life Technologies)"
/note="vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; The
NIH_BMAP_MOB_N library is a normalized library constructed
from mouse olfactory bulbs. The tag is a string of 5
nucleotides present between the Not I site and the
oligo-dT track. The library was constructed as described
by Bonaldo, Lennon and Soares, Genome Research 6: 791-806
, 1996. Tissue provided by Ms. Annie Novakovich,
Zivic-Miller Laboratories."
99 a 148 c 125 g 104 t

BASE COUNT
ORIGIN

Query Match 14.4%; Score 117.6; DB 140; Length 476;
Best Local Similarity 57.7%; Pred. No. 1.1e-22;
Matches 210; Conservative 0; Mismatches 154; Indels 0; Gaps 0;

QY 266 GCCTCTTAATAATGAGTATTCGTGTATCAACACCTGCACACGCTGGCTGCAGAAATGA 325
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Db 57 GTCGTGTTTCTAATGCTGTGCTCCGAGCCGAGCAGCAGCCTGACACAGCTGGGTGCTGACACCT 116
QY 326 TTAACAGCTTTTGGAGACAGCTTTTCCCTGAGGAACGACAGCAGCTGAGTAAATCTTCC 385
Db 117 ACAAGAGTTTCAGCGCTGCTACATCTCCGAGGAGCAGCGCTATTCCATTCAAGATGCC 176
QY 386 CTCGTCTTTTGCATTTCTGACTACATTTGAGCGGCTGCTGAGAAAGATGAAACACAGA 445
Db 177 AGGCTGCTTTCTGCTTCTCAGAGACCATCCGCGCCGCCACAGCAAGGAGGAGGCCAGC 236
QY 446 AGAGCTCTATGCTGAAGCTTCTTCGATCTCTTTTCACTCATTTGATCTCTGGAGTTCC 505
Db 237 AGAAGACCGACATGGAATGCTTCGCTTTCTCGCTGCTCATCCAGTCTGCTGGGC 296
QY 506 CAAGCAGTCCCTGAGCGGAACCGTCTCAACAGCCTGACCGTAGGGAACCCCAACAGC 565
Db 297 CGGTGAGTTCTTCCAGCAGGATTTTCAACACAGCCTGATGTTGCGCAGCTCGGACCGTG 356
QY 566 TCACGTAGAGTGGCGGACTTGAATGGGAGTGTGCTGCTATCCAGGAGTGTCTCG 625
Db 357 TCTATGAGAACTGAAGGACCTGGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 416
QY 626 ATGG 629
Db 417 ATGG 420

RESULT 12
AW330514
LOCUS AW330514 261 bp mRNA EST 01-FEB-2000
DEFINITION Ipit000097 Channel Catfish Lambda Unizap cDNA Library Ictalurus punctatus cDNA clone Pit00097 5' similar to Growth hormone, mRNA sequence.
ACCESSION AW330514
VERSION AW330514.1 GI:6826875
KEYWORDS channel catfish.
SOURCE Ictalurus punctatus
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi; Siluriformes; Ictaluridae; Ictalurus.
REFERENCE 1 (bases 1 to 261)
AUTHORS Karsi, A., Li, P., Dunham, R. A. and Liu, Z. J.
TITLE Transcriptional activities in the pituitaries of channel catfish before and after induced ovulation by injection of carp pituitary extract as revealed by expressed sequence tag analysis
JOURNAL J. Mol. Endocrinol. 21 (2), 121-129 (1998)
MEDLINE 99027338
COMMENT Contact: Liu, Z. J.
Fish Molecular Genetics and Biotechnology
Auburn University
203 Swingle Hall, Department of Fisheries, Auburn, AL 36849, USA
Tel: 334 844 4054
Fax: 334 844 9208
Email: zliu@acesag.auburn.edu
Seq primer: M13 Reverse.
FEATURES
Location/Qualifiers
1..261
/organism="Ictalurus punctatus"
/db_xref="taxon:7998"
/clone="Pit00097"
/clone_lib="Channel Catfish Lambda Unizap cDNA Library"
/dev_stage="Mature"
/note="Organ: Pituitary; Vector: Lambda vector Unizap II (Stratagene); Site_1: EcoRI; Site_2: XhoI"
BASE COUNT 64 a 66 c 79 g 52 t
ORIGIN
Query Match 14.3%; Score 117.2; DB 114; Length 261;
Best Local Similarity 72.9%; Pred. No. 1.2e-22;
Matches 191; Conservative 0; Mismatches 68; Indels 3; Gaps 3;

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QY 550 GGAACCCCCAACAGCTCACTGAGAACTGGCCGACTTGAAATGGGCATCAGTGTGCTC 609
Db 2 GGCAACCTTACCATTATCGCAGAGAAGCTGCTGACCTG-AAATGGGCATCGGCTACTT 60
QY 610 ATCCAGCATGCTCGATGGTCAACCAACATGATTAACGACTCTCTGCCGCTGCT 669
Db 61 ATCGAGGTAGTGTGTAGGACAAACCGGCTGTGTAGAGAACGACTCTCTGGCTCCGCC- 119
QY 670 TTTGAGGACTTCTTACTTGAGCATGGGGAGAACAACTCAGAGAGAGCTTTTCGTCT-GCT 728
Db 120 TTGAGGATTTCTACAGACCTTGAGCGAGGGAACCTGAGGAAGAGCTTCGCTGCT 179
QY 729 GGCTTGTCTCAAGAAGACATGCAAAAGTCGAGACCTACTTTGAGGGTTGCAAAATTGCG 788
Db 180 GTCTGTCTTCAAGAAGACATGCAAAAGTGGAGACCTATCTGAGCGTGGCCAGTGCAG 239
QY 789 GAGATCCCTGGATTCCAACTGC 810
Db 240 GAGTACTCGGTTACCAACCTGC 261

RESULT 13
AW170721/c
LOCUS AW170721 697 bp mRNA EST 29-JAN-2001
DEFINITION AU170721 Ol-br-ad cDNA Oryzias latipes cDNA clone br6604, mRNA sequence.
ACCESSION AU170721
VERSION AU170721.1 GI:12592792
KEYWORDS EST.
SOURCE Japanese medaka.
ORGANISM Oryzias latipes
REFERENCE 1 (bases 1 to 697)
AUTHORS Mita, K., Ishikawa, Y. and Yamauchi, M.
TITLE Establishment of cDNA database of medaka, Oryzias latipes
JOURNAL Unpublished (2001)
COMMENT Contact: Mita K
Genome Research Group
National Institute of Radiological Sciences
Anagawa 4-9-1, Inage, Chiba 263-8555, Japan
Email: kmita@nirs.go.jp
method: uni-directional sequence direction: sequenced from T3 primer (5' -> 3').
FEATURES
Location/Qualifiers
1..697
/organism="Oryzias latipes"
/strain="HNI"
/db_xref="taxon:8090"
/clone="br6604"
/clone_lib="Ol-br-ad cDNA"
/sex="female/male mixed"
/tissue_type="brain"
/dev_stage="adult"
BASE COUNT 173 a 149 c 170 g 204 t 1 others
ORIGIN
Query Match 14.0%; Score 115; DB 107; Length 697;
Best Local Similarity 53.2%; Pred. No. 7.1e-22;
Matches 306; Conservative 0; Mismatches 245; Indels 24; Gaps 2;
QY 251 TCTAGACAACACCGGCTCTTCAATAATGACGTCAATTCGTTGTACAAACCTGCACCAGC 310
Db 687 TCACAGACAGCCCAACGCTCTGTTGCCATTGCAGTAAGCGGTTTCAGCACCTCCACCTGC 628
QY 311 TGCTGCAAAAATGATTAACGACTTTGAGGACAGCCCTGTTGCCCTGAGGAACGAGAGAGC 370
Db 627 TCGCCAGAGACATTTTCTCTGACTTTTGAGAGTTCTCTGCAGACTTGAGGAACAAGCTCAAC 568
QY 371 TGAGTAAATCTTCCCTCTCTCTTCTGCAATTCTGACTTACATTGAGGCGGCTCTGTGAA 430

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Db 567 TCAGCAAAATCTTCTGAGGAGTCACTGTAATCTGATCAACATCAGCCCATAGACA 508
QY 431 AAGATGAACACAGAGAGCTCTATGCTGAAGCTCTCTTCGCGATCTCTTTACCTCATTTG 490
Db 507 AGCAGCGCACACAACAGTCCGGTTTCAAGAGCTGCTGTCAATTTGCTATGTTCTGGTGG 448
QY 491 AGTCTGGGAGTTCCCAAGCCAGTCCCTTGAGCGGAACCGTCTCAAAACAGCCCTGACCGTAG 550
Db 447 AATCTGGGAGTTACCCAGTCCGCTCTTTGCTGGGAGTTCTGCTCCAAGG----- 396
QY 551 GGAACCCCAACAGCTCACTGAGAGCTGGCGGACTTGAATAATGGGCATCACTGTGCTCA 610
Db 397 -----AACCAATCTCAACCAACTGGCTGACTCAAGACAGAGAAATCTTCTTCTGA 346
QY 611 TCCAGGAGTCTCGATGGTCAACCAACATGGATGATTAACGAGCTCTTGGCGCTGCC-- 668
Db 345 TCAGGGCCAAATCAGAAATAGCTAGATATATGAGACACCTGTCTTCCACCTGGGGG 286
QY 669 -----TTTTGAGGACTTCTACTTTGACCATGGGGGGAACAACTCTCAGAGAGAGCTTTCGTC 724
Db 285 AGTACATAGACTTATATCATGGACTTGGAGCCGATGGCTCACTGGCGGGAGCTACGAAAC 226
QY 725 TGCTGGCTTGGCTTCAAGAGGACATGCAAAAGTGGAGACCTACTTGGAGGGTTGCAAAAT 784
Db 225 TGCTAGCTTGTTCAGGAAGCATATGCAATAAGTGGAGACCTACCTGACTGTGGGCTAAAT 166
QY 785 GCAGGAGATCCCTGGATTCGAACCTGCACCCCTGTAG 819
Db 165 GTCGACTGTCTCCAGAGACAAACTGTATCCTGTAG 131

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RESULT 14

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LOCUS AUI67389 773 bp mRNA EST 29-JAN-2001
DEFINITION AUI67389 Ol-br-ad cDNA Oryzias latipes cDNA clone br0552, mRNA
sequence.
ACCESSION AUI67389
VERSION AUI67389.1 GI:12589458
KEYWORDS EST.
SOURCE Japanese medaka.
ORGANISM Oryzias latipes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
Belontiiformes; Adrianichthyidae; Oryziinae; Oryzias.
REFERENCE 1 (bases 1 to 773)
AUTHORS Mita,K., Ishikawa,Y. and Yamauchi,M.
TITLE Establishment of cDNA database of medaka, Oryzias latipes
JOURNAL Unpublished (2001)
COMMENT Contact: Mita K
Genome Research Group
National Institute of Radiological Sciences
Anagawa 4-9-1, Inage, Chiba 263-8555, Japan
Email: knita@nirs.go.jp
method:uni-directional sequence direction:sequenced from T3 primer
(5' -> 3').

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FEATURES

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1..773
/organism="Oryzias latipes"
/strain="HNI"
/db_xref="taxon:8090"
/clone_lib="Ol-br-ad cDNA"
/sex="female/male mixed"
/tissue_type="brain"
/dev_stage="adult"
BASE COUNT 227 a 191 c 165 g 190 t
ORIGIN

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Query Match 14.0%; Score 115; DB 107; Length 773;
 Best Local Similarity 53.2%; Pred. No. 7.3e-22;

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Matches 306; Conservative 0; Mismatches 245; Indels 24; Gaps 2;
QY 251 TCTCAGACAACAGCGGCTCTTCAATAATGTCAGTCAATTCGTGTACAAACACCTGCACGAGC 310
Db 95 TCACAGACAGCCACAGCTCTGTTGGCAATTCAGTAAGAGGGTTTCAGCACCTCCACCTGC 154
QY 311 TGGCTGCAGAAATGATTAAACGACTTTTGGAGCAGACGCTGTTGGCTTGAGGACGACGACGAGC 370
Db 155 TCGCCACAGAGACTTTTCTCTGACTTTTGAGAGTTCTCTGCAGACTGAGGAACAACGTCAC 214
QY 371 TCAGTAAATCTTCCCTCTGCTCTTTCTGCAATTCGACTACATTTGAGGCGCCCTGCTGGAA 430
Db 215 TCAGCAAAATCTTCTTGCAGGATCACTGTAACCTCTGATATCAACATCAGCCCATTAGACA 274
QY 431 AAGATGAACACAGAGAGCTCTATGCTCAAGCTCTTCTGCAATCTCTTTTCACCTCATTTG 490
Db 275 AGCAGCGCACACAACAGTCCGGTTTCAAGAGCTGCTGTCAATTTGCTATGTTCTGGTGG 334
QY 491 AGTCTGGGAGTTCCCAAGCCAGTCCCTTGAGCGGAACCGTCTCAAAACAGCCCTGACCGTAG 550
Db 335 AATCTGGGAGTTACCCAGTCCGCTCTTTGCTGGGAGTTCTGCTCCAAGG----- 384
QY 551 GGAACCCCAACAGCTCACTGAGAGCTGGCGGACTTGAATAATGGGCATCACTGTGCTCA 610
Db 385 -----AACCAATCTCAACCAACTGGCTGAACTCAAGACAGAGAAATCTTCTTCTGA 436
QY 611 TCCAGGAGTCTCGATGGTCAACCAACATGGATGATTAACGAGCTCTTGGCGCTGCC-- 668
Db 437 TCAGGGCCAAATCAGAAATAGCTAGATATATGAGACACCTGTCTCTTCCACTGGGG 496
QY 669 -----TTTTGAGGACTTCTACTTTGACCATGGGGGGAACAACTCTCAGAGAGAGCTTTCGTC 724
Db 497 AGTACATAGACTTATATCATGGACTTGGAGCCGATGGCTCACTGGCGGGAGCTACGAAAC 556
QY 725 TGCTGGCTTGGCTTCAAGAGGACATGCAAAAGTTCGAGACCTACTTTCGAGGGTTGCAAAAT 784
Db 557 TGCTAGCTTGTTCAGGAAGCATATGCAATAAGTGGAGACCTACCTGACTGTGGTAAAT 616
QY 785 GCAGGAGATCCCTGGATTCGAACCTGCACCCCTGTAG 819
Db 617 GTCGACTGTCTCCAGAGACAAACTGTATCCTGTAG 651

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RESULT 15

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LOCUS AW657301 495 bp mRNA EST 14-JUL-2000
DEFINITION 110066 MARC 1BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION AW657301
VERSION AW657301.1 GI:7423127
KEYWORDS EST.
SOURCE cow.
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidae;
Bovidae; Bovinae; Bos.
REFERENCE 1 (bases 1 to 495)
AUTHORS Smith,T.P.L., Casas,E., Stone,R.T., Heaton,M.P., Grosse,W.M.,
Bennett,G.A., Fahrenkrug,S.C., Freking,B.A., Rohrer,G.A., Laegreid
,W.W. and Keele,J.W.
TITLE Design and use of four pooled tissue normalized cDNA libraries for
EST discovery in cattle
JOURNAL Unpublished (2000)
COMMENT Contact: Smith TEL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
PCR Primers
FORWARD: AGGAACAGCTATGACCAT

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Search completed: May 16, 2001, 09:43:34
Job time: 4322 sec